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Result
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Listing first 45 summaries
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Probe #3475 for ge
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Human secreted exp	AAA45576	21	102	5.4	69	5
Zea mays DNA fragm	AAC41976	21	540	6.3	80.2	4
Human ovarian tumo	AAH83052	22	459	7.1	90.6	ū
Human secreted pro	AAC14929	21	121	9.5	121	2
Oligonucleotide D1	AAF58255	22	938	9.7	123.4	Ξ
	AAF58255	22	938	9.7	123.4	ō
	AAF58262	22	936	9.7	123.4	39
	AAF58262	22	936	9.7	123.4	8
	AAF58259	22	936	9.7	123.4	37
ര	AAF58259	22	936	9.7	123.4	36
	AAF58257	22	936	9.7	123.4	3
	AAF58257	22	936	9.7	123.4	4
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	AAF58254	22	936	9.7	123.4	2
Oligonucleotide Dl	AAF58252	22	936.	9.7	123.4	Ξ
Oligonucleotide Dl	AAF58252	22	936		123.4	õ
Trichoderma reesei	AAF14920	21	517	9.8	125.2	9
Zea mays DNA fragm	AAC44755	21	1173		144.2	8
-	AAH42526	22	1498		158.2	27
Partial cDNA seque	AAH42525	22	1243		158.2	8
#8430 u	AAI08439	22	186	13.8	176.4	Š
Probe #16754 used	AAI48068	22	186	•	176.4	4
Probe #12699 for g	AA122766	22	186		176.4	ü
Fusarium venenatum	AAF07559	21	1037		184.8	ລັ
Arabidopsis thalia	AAC33909	21	1139	14.8	189.2	12
	AAC49778	21	1136		190.8	õ
Aspergillus oryzae	AAF13899	21	1141		199.2	ြ
-	AAZ77472	20	357		202.2	ω
Human colon cancer	AAC98069	21	1215		375.8	7
Human prostate tum	AAZ52867	20	1202		375.8	6
regula	AAX89287	20	1198	•	375.8	G
gene s	AAT21836	16	416		381.2	4
#3422	AAI03431	22	411	30.4	387	ω
Probe #3590 used t	AAI34904	22	411	30.4	387	N

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## ALIGNMENTS

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disclosure; Fig lA-D; 30pp; English.	Human pyrophosphatase used in treatment and prevention of cancer -	WPI; 1999-633321/54. P-PSDB; AAY41160.	Hillman JL, Hawkins PR;	(INCT-) INCTYE PHARM INC.	31-OCT-1996; 96US-0741437.	13-AUG-1998; 98US-0134593.	09-NOV-1999. ·	US5981232-A.	Homo sapiens.		Human; pyrophosphatase; HPYP; genetic engineering; inflammatory disease;	Human pyrophosphatase (HPYP) encoding cDNA.	24-JAN-2000 (first entry)	AAZ23249;	RESULT 1 AAZ23249 ID AAZ23249 standard; cDNA; 1275 BP.

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                                                                                                                                                                                                                                        31-OCT-1996;
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                                                                                                                                                                                                                                                                                  31-OCT-1996;
                                                                                                                                                                                                                                                                                                                        01-DEC-1998
                                    DNA encoding human precombinant protein, tissue regeneration
                                                                                                                WPI; 1999-044570/04
P-PSDB; AAW70876.
                                                                                                                                                                        Hawkins PR,
                                                                                                                                                                                                        (INCY-)
  Claim 3; Fig 3A-D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inorganic pyrophosphatase; HPYP;
                                                                                                                                                                                                            INCYTE PHARM
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Best Local Similarity
Matches 1275; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human inorganic pyrophosphatase designated HPYP. Nucleic acids encoding HPYP were first identified in Incyte clone 768320 from the lung tissue cDNA library LUNGNOTO4. The recombinant pyrophosphatase, may be useful in promoting cell
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                                                                                                                                              CTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCCTGTGA
                                                             GACTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGGCCC
                                                                                                                                                                                                       TATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAG
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                                                                                                                                                                                                                                                                                                      AAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGA
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cttcaagtgtgatcctgatgctgccagagccattgtggatgctttaccaccaccctgtga
                                                gactaagaaaacgaatggaaaaggaatcagttgcatgaatacaactttgtctgagagccc
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                  WPI; 2001-502139/55
P-PSDB; AAU05122.
                                                 Hawkins
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13-AUG-1998;
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98US-0134593
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/product=
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                                                                                                                                                                                  "Human pyrophosphatase"
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New human pyrophosphatase polypeptides

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Best Local Similarity
Matches 1275; Conser
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cancer. HPYP and the vector encoding HPYP may be used to in the
regeneration or transplantation and development of nerve, pancre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation to occur. The polynucleotides may be used to detect quantify gene expression in biopsied tissues in which expression of HPYP may be correlated with a disease, for screening libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone marrow, prostate tissue and could involve supplying various natural molecules, in drug regimes that allow cell division and differentiation to occur. The polynucleotides may be used to detect
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                      tggctgttgtggtgacaatgacccaattgatgtgtgtgaaattggaagcaaggtatgtgc
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compounds for various drug screening
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## RESULT AAX00685

ΧIJ AAX00685 standard; DNA; 1351

25-MAR-1999 (first entry)

Human secreted protein gene 75 clone HOSEI45

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; thymus; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; Human; Sected Far--- diagnosis; tissue; cancer; tumour; neurodeyemetric; blood; allerg developmental abnormality; foetal deficiency; blood; allerg developmental abnormality; foetal deficiency; brain; hepatic; endocrine; metabolism; regulation; developmental abnormality; roctal deficiency immune system; asthma; lymphocytic disease; immune system; asthma; lymphocytic disease; secreted protein; fusion protein; otein; gene therapy; protein therapy; neurodegenerative disorder; leukaemia; deficiency; blood; allergy; renal; ds; malabsorption; lymphoma;

Homo

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21-MAR 1997
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                                                                                                                                                                                                            secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX06611-X00724; amino acid sequences AAX67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and useful for diagnosis and trodisorders, immune diseases,
                                                                                                                                                                                 Sequence
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P-PSDB;
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This sequence secreted human
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Greene JM,
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                                               New isolated human genes and the secreted polypeptides they encouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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The invention relates to 87 novel genes and their fragments (nucleic The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611.7x00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides in a sample or by determining the presence of mutations in polypeptides in a sample or by determining the presence of mutations in polypeptides in a sample or by determining the presence of mutations in polynucleotides, based on which tissues they are most highly expressed polynucleotides, based on which tissues they are most highly expressed
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gene therapy; treatment;
                                                                                                                                                                                                                                                                      Human ovarian
                                                                                                                                                                      09-APR-1998;
                                                                                                                                                                                                                                                                                         10-APR-2000
This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The producti
                                                  New nucleic acid sequences expressed in
tissues, and derived polypeptides, for
identification of therapeutic agents
                                                                                                                                 (META-) METAGEN GES GENOMFORSCHUNG
                                                                                                                                                   09-APR-1998;
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                                   Claim
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CC of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete (C) genes. (B) are used (i) to identify agents suitable for treatment of (C) covarian cancer; (ii) directly for treating this form of cancer (c) including expression from gene therapy vectors) and (iii) for generation (C) fixed antibodies. (A) are identified by assembling ESTS (expressed (C) expression patterns. This allows a significantly longer fragment of the (C) gene to be revealed, so should reduce the number of failures associated (C) with the fact that ESTS from different libraries may represent different (C) parts of the same unknown gene, distorting the estimated frequency of (C) covarian tumor cDNA library derived EST fragments described in the method (C) covarian tumor cDNA library derived EST fragments represented in (C) (C) AAY76505-Y76638.
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Sequence 856 BP; 251 A; 163 ç 222 G; 220 T; 0 other

DB 20;

Length

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                                                   aatgatgtcaaacggctgaaacctggctacttagaagctactgtggactggtttagaagg
                                                            AATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGG
                                                                                  gactggaaagtcattgccattaatgtggatgatcctgatgcagccaattataatgatatc
AAGGACTTTGCCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGACT
                             TATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGAT
                       tataaggttcctgatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaaagat
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                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
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 677 GATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACTTTGCC
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                                  CGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCT 676
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                      cggctgaaacctggctacttagaagctactgtggactggtttagaaggtataaggttcct
                                                                               Similarity
                                                                                                                                                             used to
                                                                                                                             660 BP;
                                                                                                                                                                                                                                                                                                                      SEQ ID 14703;
                                                                                                                                                  and secretion
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping;
                                                                                                                                                           forensic, gene therapy and chromosome mapping procedures to obtain upstream regulatory sequences and to design
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Pred. No. 4.5e-177;
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to 5'ESTs and for
e mapping procedures
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AAA78135/c
ID AAA78135
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02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
02-DEC-1999;
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WPI; 2000-442671/38
                                                                                                                                                                                                                                                                                                             Human colon tumour polypeptide; tumour antigen; immunotherapy; diagnosis; progression; ss.
                                                                                                                                                                                                                                                                                                                                                        cDNA encoding
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                              Wang T,
                                              Xu J,
                                                                                                                                                                                              23-DEC-1999;
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                                                                         (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                       human colon tumour polypeptide,
                                                                                                    99US-0401064.
99US-0444242.
99US-0454150.
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99US-0347496
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                                              Secrist
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                                           H,
                                              Benson
                                              DR,
                                            Meagher
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Claim 1; Page 212; New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the 229pp; English

portions of proteins which are associated with human colon tumours. The invention also specifically discloses 8 human colon tumour proteins (AABI1897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, such polypeptides may be used in vaccines that target tumour cells such polypeptides are cancer. T-cells specific for the polypeptide expressed by the APC are cancer. T-cells specific for the polypeptide expressed by the APC are used to remove tumour cells from biological samples, especific for the fractions thereof. The sample or the isolated T-cells specific for the fractions thereof. polypeptide can then be used to inhibit cancer development. CD4+ and/or CD8+ T-cells from a patient may be incubated with a polypeptide or nucleic acid of the invention, or an APC expressing such a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be cloned and then administered back to the patient to inhibit cancer development. Nucleic acids encoding the polypeptides and antibodies against the polypeptides may be used to determine the expression level against the polypeptides may be used to determine the expression level of a tumour protein of the invention, and therefore to determine whether. Sequences AAA77722-A78199 represent 478 cancer cells are present. Such diagnostic methods may also be used to monitor the progression of a cancer by repeating the processes at time intervals, and comparing the current result to previous results. The present sequence represents a cDNA encoding a human colon tumour cDNAs encoding proteins o R

Sequence 578 вp; 155 A; 139 c; 99 G; 185 T; 0 other;

Similarity

44.0%; 99.1%;

Length 578;

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99
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                                                                                                              AGAAGCTACTGTGGACTGGTTTAGAAGGTATAAAGGTTCCTGATGGAAAACCAGAAAATGA 696
                                                                                                                                                  TCCTGATGCAGCCAATTATAATGATATCAATGATGTCAAACGGCTGAAACCTGGCTACTT 636
                                                                        ATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGGATGA
                                                                                                                                                                                                   ATTGCCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGGATGA
                                                                                                                                                                                                                               GAATACAACTTTGTCTGAGAGCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGT
                                  TCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGAATGGAAAAGGAATCAGTTGCAT
                                              TCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGAATGGAAAAGGAATCAGTTGCAT
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                               Score 560.6; DB 21;
pred. No. 3.6e-149;
0; Mismatches 4;
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Sequence

BP; 155 A; 139 C;

99 G;

185 T; 0 other;

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RESULT, 10
AAI28873/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 FEB-2000;
06-MAR-2000;
19-MAY-2000;
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                                                                                                                                                                       activity of TCAPs by expressing inactive proteins or to supplement the activity of TCAPs by expressing inactive proteins, (II) may be used to patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and polymerase chain reaction (PCR) and hybridisation assays to detect and polymerase chain reaction for similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may therefore which patients may be in need of restorative therapy. (TCAPs also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1999;
10-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colon tumor associated proteins and prevention, diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                              used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression, such as colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with inappropriate colon tumour associated protein (TCAP) associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be expression, such as colonic cancer. For example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the polynucleotides (II) that encode them. (I) have cytostatic activity (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases (II) may be used in the prevention, diagnosis and treatment of diseases
                                                             as diagnostic agents for detecting the presence of TCAPS in Sa (e.g. by enzyme linked immunosorbant assay (ELISA)). AA128460 and AAM24494 to AAM24523 represent nucleotide and amino acid s
                                                                                                                 Anti-(I) antibodies and antagonists may also be used to down regulate Anti-(I) antibodies may also be used TCAP expression and activity. The anti-(I) antibodies may also be used TCAP expression and activity the presence of TCAPs in samples as diagnostic agents for detecting the presence of TCAPs in samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Page 249; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0575251.
; 2000US-0609448.
; 2000US-0649811.
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Jiang Y;
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04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #3475
                                                                                                                                                                                                                                                                                                                                                                                                              human; microarray; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                       cancer;
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                for gene expression analysis in human cervical cell sample
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                                                                                                                                                                                                                                                                                                                                                                                                              cervical epithelial cell;
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RESULT 12 AAI34904/c

AAI34904

standard;

DNA;

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XXX DT XXX

17-OCT-2001

(first entry)

genetic disorder;

Probe; microarray;

human;

placenta; antenatal

Probe #3590 used to measure gene expression in human placenta

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04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray, which can be used for measuring human gene expression in sample derived from human cervical epithelial cells. By measuring gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 411 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression, the probes are therefore useful in grading and/or
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                                                                                                                                                                                                                                                AAGACCCAGGGCACAATGATAAAACATACTGGCTGTTGTGGTGACAATGACCCCAATTGATG 452
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               ACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCTGATGGAA
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 ACTTAGAAGCTACTGTGGACTGGGTTAGAAGGTATAAGGTTCCTGATGGAA
                                                        ATGATCCTGATGCAGCCAATTGTAATGATATCAATGATGTCAAACAGCTGAAACCTGGCT
                                                                        ATGATCCTGATGCAGCCAATTATAATGATATCAATGATGTCAAACGGCTGAAACCTGGCT
                                                                                                                   GCATATTGGCTATGATTGACAAAGGGGAAACTAACTGGAAAGTCATTGCCATCAATGTAG
                                                                                                                                  GCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGG
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Homo sapiens

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Matches 39
                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                    Human genome-derived single analyzing gene expression in
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                                                                                                                                                                                                                                                          Sequence 411 BP; 106 A; 101 C;
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                                                                171
 51
                                                                                                                                                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                             2001-488897/53
                                                                                            GCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGG
                                                                                                                          AAGACCCAGGGCACAATGATGAACATACTGGCTGTTGTGGTGACAGTGACCCAATTGATG
                                                                                                                                  AAGACCCAGGGCACAATGATAAACATACTGGCTGTTGTGGTGACCAATGACCCAATTGATG
ATGATCCTGATGCAGCCAATTATAATGATATCAATGATGTCAAACGGCTGAAACCTGGCT 632
                                                               GCATATTGGCTATGATTGACAAAGGGGAAACTAACTGGAAAGTCATTGCCATCAATGTAG
                                ATGATCCTGATGCAGCCAATTGTAATGATATCAATGATGTCAAACAGCTGAAACCTGGCT
                                                                                                                                                                                                                      396;
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                        SEQ ID No 3590; 654pp;
                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US00663
                                                                                                                                                                                                                              30.4%;
                                                                                                                                                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                        in human
                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                                                                                                                                                                                                                                                             exon nucleic acid
                                                                                                                                                                                                                      Score 387; DB 22;
Pred. No. 5.8e-100;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                            67 G; 137
                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                        placenta
                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                                                              T; 0 other;
                                                                                                                                                                                                                                                                                                                                                probes useful for
                                                                                                                                                                                                                                       Length 411;
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                      ng gene
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                           352
                                                                                                                                                                                                                                                                                      useful
                                                                                   572
                                                                                                  172
                                                                                                                                               452
                                                                                                                                                                            392
                                                                                                                               232
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RESULT 13 AAI03431/c ID AAI03431

standard; DNA;

411

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Query Match
Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe; human; breast disease; breast cancer; development disorder;
inflammatory disease; proliferative breast disease; non-carcinoma t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI03431;
                                                                                                                                                                                                                                                                                                                                                                        breast. The probes are useful for predicting, diagnosing, grading staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The disease include: breast cancer, disorders of development, inflammatory dof the breast, fibrocystic changes, proliferative breast disease non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                             measuring human gene expression in a human breast sample, where the property human breast sample, where the property is a nucleic acid expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a .human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                            273 CAAAGGACCCTTTAAACCCTATTAAACAAGATGTGAAAAAAGGAAAACTTCGCTATGTTG
                                                                                                                     351
                                                                                                                                               333
                                                                                       393
   231
                              453
                                                          291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to novel single exon nucleic ac
present sequence is one such probe. The probes are useful
suring human gene expression in a human breast sample, when
                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #3422 used to
                                                                                                                  396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 3422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US00661
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                           106 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                   30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen · W,
                                                                                                                                                                                                                                                                                                            101 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                     Score 387; DE Pred. No. 5.8e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                            G;
                                                                                                                                                                                                                                                                                                              137 T; 0 other;
                                                                                                                                                                                                                                           DB 22;
5.8e-100;
hes 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measuring
                                                                                                                                                                                                                                                                    Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                  breast disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                       part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                              The diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                  diseases
                                                                                                                                                                                                                                           Gaps
                                                                                                  452
                                                                                                                              292
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851

Matches

405;

Conservative

0

Mismatches

8

Indels

2:

Gaps

2

60 910

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RRESULT 1
RAT2118 ANT218
IID ANT22
XX ANT22
XX ANT22
XX Gene
KW Gene
KW Huma
XX Homc
XX Hom
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                           3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                           A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene signature HUMGS03377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT21836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT21836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 977; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OKUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MATS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                 ences were obtained from 3'-directed cDNA libraries prepared various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signature;
n; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCTGATGGAA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCATTAATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUBARA K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       окиво
                                                       different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             re; messenger RNA; mRNA; relativ ng; mapping; non-biased library; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA to mRNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relative abundance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frequency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g
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RESULT :

15

AAX89287

standard; DNA; 1198

ВP

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361

1211

GTGCAAGG-GGAGCACATATTGGATGTATATG-TTACCATATGTTAGGAAATAAA 1263

gtgcaaggccgngcacatattggntgtatatgtttnccntatgttaggggataaa

415

CTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGAT

cttttagcacatgcttaaatatcaaagcagttgtcatttggaagtcacttgtgaatagat

AATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAA 1150

aatccaatatactcagaatgttatccatctaaagcatttttcatatctcaactaagataa

300

agcttttcaaagctttaaatttgtagaactcatcttaactaaagtaaattctgctgtgact

ggaatacangctgatattgctacatcgtgttcatctggatgtattagaagtaaaagtagt GGAATACAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGT acagtaccaacagacgtggataagtggttccatcaccagaaaaactaatgagatttctct

180 1090

240

1030

301

1151

241

Qy

1091

В δÃ B

181

1031

Ωy Вb Qy В

971

121

911

ACAGTACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCT

<u>بــ</u>

61

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cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; tetracarcinoma; Addison's disease; adult respiratory distress syndrome; allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus; Crohn's disease; ulcerative colitis; atopic dermatitis; dermatomyositis; diabetes mellitus; emphysema; atrophic gastritis; glomerulonephritis; gout; Grave's disease; hypersinophillia; irritable bowel syndrome; AIDS
                                                                                                                                                                                                                                                                                    lupus erythematosus; multiple sclerosis; myasthemia gravis; infarction; osteoarthritis; osteoporosis; pancreatitis; polymyositis; hemodialysis;
                                                                                                                                                                                                                                                                        arthritis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                   Regulatory protein; HRGP; human; cell proliferation; immune response;
                                 P-PSDB;
                                                                                Au-young
                                                                                                        (INCY-) INCYTE
                                                                                                                                  31-DEC-1997;
                                                                                                                                                          22-DEC-1998;
                                                                                                                                                                                  08-JUL-1999
                                                                                                                                                                                                          W09933870-A2
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                 1999-430229/36.
DB; AAY28917.
                                                                                                                                                                                                                                                                                                                                                                                                             regulatory
                                                                     g J,
Shah
                                                                    Bandman O,
P, Tang Y
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                          PHARM
                                                                                                                                 97US-0001403
                                                                                                                                                        98WO-US27471
                                                                                                                                                                                                                                                                                                                                                                                                             protein HRGP-3 encoding DNA
                                                                     ΥT,
                                                                                                                                                                                                                                                                        Sjoegren's
                                                                     Corley NC,
Yue H;
                                                                                                                                                                                                                                                                        syndrome;
                                                                                  Guegler
                                                                                                                                                                                                                                                                        and
                                                                                  S
                                                                                                                                                                                                                                                                        autoimmune
                                                                                  Hillman
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thyroiditis

AIDS;

Query Match Best Local Similarity

29.98;

Score Pred.

381.2; DB 16; No. 2.6e-98;

Length

416;

New human regulatory proteins, useful for diagnosing, preventing and treating disorders associated with expression of regulatory proteins

Sequence 416

BP;

128 A; 77

Ç

77 <u>ن</u>

128

H 6 other

Claim 3; Page 82; 89pp; English.

CC metanoma, myeloma, sarcoma, and tetracarcinoma. Such cancers include, contain, cervix, breast, gall bladder, ganglia, ovary and pancreas. Where cc brain, cervix, breast, gall bladder, ganglia, ovary and pancreas. Where cd decrease the activity of HRGP are administered. Such responses may be cd ssociated with disorders such as Addison's disease, adult respiratory cc distress syndrome, AIDS, allergies, anemia, asthma, atherosclerosis, cc dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic cc dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic cc diritable bowel syndrome, lupus erythematosus, multiple sclerosis, cc osteoporosis, poncreatitis, polymyositis, rave's disease, hypersinophillia, cc osteoporosis, pancreatitis, polymyositis, rational artitis, crave's disease, hypersinophillia, cc osteoporosis, pancreatitis, polymyositis, rational artitis, cc osteoporosis, pancreatitis, polymyositis, rational artitis, cc osteoporosis, pancreatitis, polymyositis, rationatod artitis, cc complications of cancer, hemodialysis, extracorporeal circulation; viral, cc bacterial, fungal, parastitic, protozoan, and helminthic infections; and cc conditions, and as a source of primers and probes. The invention provides novel human regulatory proteins (AAY28915-926), designated HRGP, and their polynucleotides (AAX89285-296). The proteins can be produced using standard recombinant technology. The expression of HRGP is closely associated with cell proliferation and the polypeptides and polynucleotides are useful in the diagnosis, treatment and prevention of diseases associated with cell proliferation, particularly prevention of diseases associated with cell proliferation, particularly prevention of prevent a cancer. The protein or agonists may be administered to treat or prevent a cancer such as adenocarcinoma, leukemia, lymphoma, mollancems amount of the cancer such as adenocarcinoma, leukemia, lymphoma, mollancems.

Sequence 1198 BP; 377 A; 227 C; 266 G; 328 T; 0 other;

dd V	Db Qy	Db Qy	Оy	Qy Db	Db Qy	Db Qy	Оγ	Qy Db	Que: Bes: Mat
641 GCTACTGTGGACTGGTTTAGAAGGTATÀAGGTTCCTGATGGAAAACCAGAAAATGAGTTT 700 			461 ATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTG 520   1		341 TTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCA 400	281 CCTTTAAACCCTATTAAACAAGATGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTG 340 		161 AAAGGACAATATATATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTT 220   1	Query Match 29.5%; Score 375.8; DB 20; Length 1198; Best Local Similarity 69.6%; Pred: No. 1.6e-96; Matches 509; Conservative 0; Mismatches 222; Indels 0; Gaps

Job time: 1442 sec

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patent; WO 9953040-A 272 21-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER
(DE); PILARSKY CHRISTIAN (DE)
Location/Qualifiers
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Direct Submission
Submitted (17-NOV-2000) National Institutes of Health, Mammalian Submitted (16, NGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer 
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BC001022.1
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                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Tiongson, E.E.,
Zhang, L.-H. and
                                                                                                                                                                                                  Gaithersburg, Maryland;
                                                                                                                                                                                                                       DNA Sequencing by: Nation Sequencing Center (NISC),
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                      McDowell,J., Pearson,R., Snyder,B.,
Tiongson,E.E., Touchman,J.W., Tsurge
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                                        GTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAG
                            GTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCG
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/protein_id="AAHO1022.1"
/protein_id="AAHO1022.1"
/db_xref="G1:12654395"
/translation="MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKDVF/translation="MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKDVFEHMVVEVPRWSNAKMELAFKDFDLXPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWEDGHNDKHTGCCGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAIN
DDGHNDKHTGCCGDNDPIDVCEIGSKVCARGEIGVKVLGILAMIDEGETDWKVIAIN
VDDPDAANYNDIMDVKRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MGC:1221 IMAGE:3345496"
/tissue_type="Lymph, Burkitt lym
/clone_lib="NIH_MGC_8"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTDVDKWFHHQKN."
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); Mismatches
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Eukaryota; Metazoa; Chordata; Cr
Eukaryota; Eutheria; Primates; Ca
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1282)
Gu,Y., Peng,Y., Li,Y., Fu,S., Gu
Han,Z., Wang,Y., Chen,Z. and Fu,
Direct Submission
Submitted (12-JAN-1999)
Shanghai, Guo Shoujing F
                               2 (bases 1 to 1282)
Huang,C., Zhang,C., Wu,,
Li,Y., Han,Z., Wang,Y.,
                                                                 Unpublished
                                                                             novel gene expressed
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inorganic
                                 Wu, T., Peng, Y., Y., Chen, Z. and
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                                 Gu,Y.,
Fu,G.
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            Human Genome
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TTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 99.1%; Score 1264; DB 9;
Similarity 100.0%; Pred. No. 2.7e-282;
64; Conservative 0; Mismatches 0;
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/product="inorganic pyrophosphatase"
/protein_id="ARP17222.1"
/db_xref="GI:6563256"
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Location/Qualifiers
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78. .947
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/db_xref="taxon:9606"
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                                                                                                            Submitted (25 MAY-1999) Molecular Cardiology Laboratory, Northwestern Healthcare Research Institute, 2650 Ridge A
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Patejunas, G.
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                                                                       Location/Qualifiers
1. .1243
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Eutheria;
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1. .1243
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/EC_number="3.6.1.1"
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Homo sapiens SID6-8061 mRNA for pyrophosphatase,
AB026723
                                                                                                                                                                                                                                                                                         Submitted (26-APR-1999) to the DDBJ/EMBL/GenBank databases. Toshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group; Anagawa 4-9-1, Inage-ku, Chiba 263-855 Japan (E-mail:t_saito@nirs.go.jp, Tel:81-43-206-3135,
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HMVVEVPRWSNAKMEIATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWE
DPGHNINKHTGCCGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGFTDWKVIAIN
VDDPDAANYNDINDVKRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAID
IIKSTHDHWKALVTKKTNGKGISCMNFTLSESPFKCDPDAARAIVDALPPCESACTV
PTDVDKWFHHQKN"
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89 ATGAGCGGCTTCAGCACCGAGGAGCGCGCGCGCGCCCTTCTCCCCTGGAGTACCGAGTCTTC 148
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                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-DEC-1999) Clinical Virology, Karolinska Institute, Huddinge University Hospital, Stockholm S-14186, Sweden Location/Qualifiers
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Kanni,L., Johansson,M. and Karlsson,A
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning of a human inorganic pyrophosphatase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kanni,L.,
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                                Similarity 99.9
86; Conservative
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                                                                                                                                                                                                                                            codon_start=1
/product="inorganic pyrophosphatase 1"
/------in id="AAG36780.1"
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                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                        IIKSTHDHWKALVTKKTNGKGISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTV
                                                                                                                                                                                                                                                                                                            'gene="PPA1"
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TAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGA
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                                              GTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAA
                                                           GTGACAATGACCCAATTGATGTGTGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAA. 491
                                                                                                                   GTGCCATCCCTCAGACTTGGGAAGACCCCAGGGCACAATGATAAACATACTGGCTGTTGTG
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 167012)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
          Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
On Apr 20, 2001 this sequence version replaced gi:77088
                                                          2: (bases 1 to 167012)
DOE Joint Genome Insti
                                                                                Unpublished
                                                                                                                                                       Homo sapiens
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HTGS_PHASE1; HTGS_DRAFT;
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pieces.
 Center
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                                                                                             Chromosome
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5 c
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                                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                              HTGS_ACTIVEFIN
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20-APR-2001 G DRAFT SEQ

SEQUENCE

Euteleostomi;
; Homo.

DOE Joint 94598, USA

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FEATURES
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Best Local
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                                                        CAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCTAATGCAAAAATGG
                                                                                                                              TCTTCCTCAAAAATGAGAAAGGACAATATATATCTCCCATTTCATGATATTCCCAATTTATG 203
                                                                                                                                                                                GCACCATGAGCGGCTTCAGCACTGAGGAGCGCGCCCACGCCCTTCTCCCCTGAAGTACCGAG
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                                     CAGATAAGGATGTGTTCCACGTGGTAGTTGAAGTACCACTGTGGTCTAATGCAAAAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center Project Name: 303711
Center clone name: CIT-HSPC_308K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Estimated insert size: 166212; sum-of-contigs estimation Quality coverage: 8.74 in Q20 bases; pulse field gel estimation Quality coverage: 8.52 in Q20 bases; sum-of-contigs estimation. * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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39820 c 39446 g 43467
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/db_xref="taxon:9606"
/chromosome="5"
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RESULT 1 AC021159

DEFINITION

AC021159 213025 bp DNA HTG 19-JUN-2000 Homo sapiens chromosome 5 clone RP11-536N17, WORKING DRAFT SEQUENCE, 41 unordered pieces.

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             ACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTTTGCT 1274
                                                CAGAACATTACCCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTTTCAGCACGTG
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 ACATATTGGATGTATGTTACCATATGTTAGGAAATAAAATTATTTTGCT
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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Waterston, R.H.
Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 213025)
Waterston, R.H.
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AC021159.4 GI:8572521
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                144
                                                  204 CAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCTAATGCAAAAATGG 263
264 AGATTGCTACAAAGGACCCTTTAAACCCTATTAAACAAGATGTGAAAAAAAGGAAAAACTTC 323
                                                                                                                                                                                  84 GCACTATGAGCGGCTTCAGCACCGAGGAGCGCGCGCGCCCTTCTCCCCTGGAGTACCGAG 143
                                                                                                                                                                                                                                                     TCTTCCTCAAAAATGAGAAAGGACAATATATATCTCCATTTCATGATATTCCAATTTATG 203
                                                                                                                                                                 GCACCATGAGCGGCTTCAGCACTGAGGAGCGCGCCACGCCCTTCTCCCTGAAGTACCGAG 75692
                                                                                                TCTTCCTCAAAAATGAGAAAGGACAATATATGTCTCCATTTCAAGATATTCCAATTTATG 75752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_name:Contig37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig36" 3616. 37205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "assembly_name:Contig41
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A6360
                                                                                                                                                                                                                                                                                                                                                                                       "assembly_name:Contig60"
| 208210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "assembly_name:Contig48"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "assembly_name:Contig46"
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                                                                                                                                                                                                                                                                                                 Score 1123.8; DB 2;
Pred. No. 1.2e-249;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                   [y_name:Contig61"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ly_name:Contig59"
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AC011012 LOCUS DEFINITION

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AC011012 155645 bp DNA HTG 03-NOV-2000 HOMO sapiens clone RP11-8D23, WORKING DRAFT SEQUENCE, 7 unordered

	24 ACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTTTGCT 1274 [	Oy 12 Db 767	
1223 76765	64 CTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGATGTGCAAGGGGAGC	Qy 11 Db 767	
1163 76705	CCATCTAAAGCATTTTCATATCT 	Qy <sub>.</sub> 11 Db 766	
1103 76645	44 TITAAATITGTAGAACTCAICTAAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACT	ОУ 10 Db 765	
1043 76590	84 ATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGTAGTAGCTTTTCAAAGC	Qy 9 Db 765	
983 . 76531	ACT ACT	Oy 9	
923 76471	364 CCAGAGCCATTGTGGGATGCTTTACCACCACCCTGTGAATCTGCCTGC	Qy 8 Db 764	
863 .76411	04 GAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCTTCAAGTGTGATCCTGATGCTG	Qy 8 Db 763	
803 76351	44 TTATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAAAGGAATGGAAAAG	Qy 7 Db 762	
743 76291	84 AACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACTTTGCCATTGATA	Оу 6 Db 762	
683 76232	24 AACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCTGATGGAA	Qy 6 Db 761	
623 76172	64 TTAATGTGGATGATCCTGATGCAGCCAATTATAATGATATCAATGATGTCAAACGGCTGA 	Qy 5 Db 761	
563 76112	04 AAGTTCTAGGCATATTGGCTATGACTTGACGAAGGGGAAACCGACTGGAAAGTCATTGCCA	Оу 5 рь 760	
503 76052	44 CAATTGATGTGTGTGÄAATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATTGGCGTGA 	Qy 4 Db 759	_
443 75992	aagacccaggggacaatgataaacatactggctgttgtggt 	Qy 3 рь 759	
383 75932	24 GCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTC	Qy 3 Db 758	_
75872		Db 758	

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 3, 2000 this sequence version replaced gi:7239549.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 12.1 in Q20 bases; agarose-fp Quality coverage: 11.9 in Q20 b.

NOTE: This is a 'vorking draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 15369 bases at least Q40
Consensus quality: 15447 bases at least Q30
Consensus quality: 154815 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 155645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 152000; agarose-fp Insert size: 155045; sum-of-contigs
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                                                                                                                                      3181
                                                                                                                                                                                                                                         2404
                                         100 b
3180: contig of 677
11 3280: gap of 100 bn
1 4042: con++-
                                                                                                                                                      2403: contig of 661 bp in 2503; gap of 100 bp 3180: contig of 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242: gap of
889: cr
                                                                                                                                                                                                                                                                                                                                                                                                                                              989:
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                                                                                                                                                                                                                                                                                                  .. yap of 100 bp in length 889: contig of 647 bp in length 100 bp 1642: contig of 653 bp in length 2: gap of 100 bp 2403: contig of 653 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center
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                                    contig
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                           ATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGA 661
                                                                                                                                                                              GGCTGTTGTGGTGACAGTGACCCAATTGATGTGTGTGAAATTTGGAAGCAAGGTATGTGCA
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/clone="RP11-8D23"
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inorganic pyrophosphatase.
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                                                                                              Molecular cloning and functional expression mammalian inorganic pyrophosphatase J. Biol. Chem. 267, 24641-24647 (1992)
                                                                                                                        1 (bases 1 to 1266)
Yang, Z. and Wensel, T.
                                                                                                                                                           Bos taurus
Eukaryota; Metazoa; Chordata;
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                                    396
                                                                                                                                                                                                            inorganic pyrophosphatase
                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="retina"
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Rumsfeld, J., Ziegelbauer, K. and Spaltmann, F.
Rumsfeld, J., Ziegelbauer, K. and Spaltmann, F.
Cloning, expression, affinity purification and characterization of polyhistidine-tagged cytosolic Saccharomyces cerevisiae and human inorganic pyrophosphatases for differential screening of compounds
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Submitted (20-NOV-1998) Research Antiinfectives
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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EverwsnakmeiatkdpelnfikgDvkkgklryvanlfpykgyimnygaipqtwedpgh
ndkhtgccgdndpidvceigskvcargeiigvkvlgilamidegetdwkvlainvddp
daanvndindvkrlkegylbarvdwfrrykvpdgkpenefafnæfkdkofaidiiks
Thdhwkalvtkktngkgiscmnttlsespfkcdpdaaraivdalpppcesactvptdv
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/protein_id="AAD24964.1"
/db_xref="GI:4583153"
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NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
                                             Direct Submission

Submitted (10-JUL-2001) National Institutes of Health, Mammalian Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1243)
                                                                                                                                                                                                                                                                                                IMAGE:3585780, mRNA, complete BC010468
                                                                                                                                                                                                                                                                              GI:14714656
                                                                                                                                                                                                                                                                                                                                       p mRNA
cDNA 2010317E03
                                                                                                                                                                                                                                                                                                                     cds
                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                       gene,
                                                                                                                                                                                                                                                                                                                                       ROD 12-JUL-2001
, clone MGC:6716
                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                              Murinae;
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AAAGGGTATATTTGGAACTACGGCGCCATCCCTCAGACATGGGAAGACCCAGGACACAGT
                                         AAAGGATATATCTGGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCCAGGGCACAAT 409
                                                                                                             CCTATTAAACAAGATGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCCCGTAT:349
                                                                                                                                                                                                                                                                                             TATATATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTA 229
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                                                                                        CCAATCAAGCAAGATGTGAAAAAGGGGAAGCTCCGCTATGTGGCGAATCTGTTCCCCTTAT
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: Baylor College of Medicine Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 10 Row: f Column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk,
A.M., Holloway, M., Telford, B, Hodgson, A., Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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DPGHSDKHTGCGGNNEPIDVCEIGSKYVCARGEIIRVKYLGILAMIDEGEFKNEFKNUFFAVD
VDDPDAANYKDISDVERLKPGYLEATVDWFRRYKVPDGKPENEFFNAEFKNUFFAVD
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/clone_iib="NCI_CGAP_Mam1"

/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="MGC:6716 IMAGE:3585780"
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/db_xref="GI:14714657"
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82.7%;
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ouck, J., Yu, W.,
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GTCATTTGGAAGTCACTTGTGAATAGATGTGCAAGGGGAGCACATATTGGATGTATATGT 1242
                                                                                     TAGACACCTCACATCTCAACCAAGACAGCTTTTATTA-AACCTTAGCTCTCAAAGCCGTG
                                                                                                  T----TCATATCTCAACTAAGATAACTTTTAGCACATGCTTAAATATCAAAGCAGTT
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US-09-134-246-8
US-08-513-9748-35
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INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Hillman, J
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                                                                                                                                                                         LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy.J.
REGISTRATION NUMBER: 36,749
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MEDIUM TYPE: Diskette
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                                                                                                                                 CTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCACCCTGTGA
                                                                                                                                                                                                                                                                                                                 TATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAG
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ATCTGCCTGCACAGTACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATG
                                            AGATTTCTCTGGAATACAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAG
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US-09-134-593-2
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                                                                       Query Match
Best Local S
Matches 1275
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APPLICANT: Hawkins,
APPLICANT: Hillman,
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
                                                                          Local Sinhes 1275;
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                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rele-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
ETLING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
 1403
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                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261
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CLONE: pTZgpt-
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261
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APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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AAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACT 548
                                                     GTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTG
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1800 Diagonal Road,
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                                                                                                                          Score 51; DB 1; Pred. No. 0.00019;
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US-08-809-267-9
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Query Match
Best Local Similarity
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                                                                                                                                                           NFORMATION FOR SEQ ID NO:
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                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1283
                                                                                                                                                                                    TELEPHONE: (508) 927-5054
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/809, 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1163
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D
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                                                                                                                                                                                                                               REGISTRATION NUMBER:
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                                                                                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
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                                                                                                            : 531 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Floppy disk
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                                                                                                                                                                          (508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEARS, Lauren E
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                                                                     DNA (genomic)
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                                                                                                  double
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3.1%;

Score Pred.

39.2; DB No. 0.1;

Length 531;

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425 TGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCCAAGGTATGTGCAAGA 484

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187 TGGTACGATGATGACGACCCGTTTGACATCATGGTCATAATGAGGGAGCCAACATATCCG 246

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   Query Match
Best Local S
Matches 95
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                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NETELECOMMUNICATION INFORMATION: (508) 927-5054
                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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ADDRESSEE: NEW ENGLAND BIOLABS,
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                Local Similarity
                                                                                                                     TOPOLOGY:
                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                     unknown
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                  DNA (genomic)
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Barton E.
                  3.1%;
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                  Score 39.2; D
Pred. No. 0.1;
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                                 DB 5;
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Query Match 2.9%;
Best Local Similarity 47.8%;
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 5
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                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
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STREET: 310
STRY: Raleigh
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9 FILING DATE: 14-DEC-1995
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                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                          LOCATION:
                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                  AGENT INC.
Kenneth D Sibley
Kenneth D Sibley
FA
                                                                                                                                                                                                                                                        1155 base pairs
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Stratton, Michael R
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500..655
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                                                                                         CDS
500.
                                                                                                                                                                                                           linear
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SYSTEM: PC-DOS/MS-DOS
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Plaza, 3605 Glenwood Avenue,
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Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
                                                                                                                                                                                                                                                                                                                                                                                        GB 9617961.9
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Score 37.6; DB Pred. No. 0.44; O; Mismatches
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Best Local Similarity Matches 122; Conserv
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                                                                                              HYPOTHETICAL:
ANTI-SENSE: 1
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                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 10-SEP CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC+DOS/MS
                                                                                                                                            TOPOLOGY:
                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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California
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Miller, Louis H
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PatentIn Release #1.0,
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   Conservative
                                                                                                                                            linear
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BINDING DOMAINS FROM PLASMODIUM VIVAX
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Score 36.8; DB Pred. No. 3.1; 0; Mismatches
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16th Floor
                               DB 2;
   142;
                                 Length 19124;
   Indels
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US-08-568-459A-3
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                               TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                        MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/568,459A
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California
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Miller, Louis H
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   Conservative
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                                                                                                        Plasmodium falciparum
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                2.8%;
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                Score 36.2; Di
Pred. No. 2.2;
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                                                                                                                       Query Match
Best Local Similarity
                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                           2286 AAGTAAAGGATGTACCAATTTCTATAATAAGAAATAATGAACAAACTTCGCAAGAAGCAG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                              MOLECULE TYPE:
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780 TGACTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGACC 839
                                                                          720 AAGATAAGGACTTTGCCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGCATTAG 779
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13, AL
NO. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92660
                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08487826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                         4507 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sim, Kim L.
Chitnis, Chetan
Chiller, Louis H.
Miller, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wellems, Thomas E.
VENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
VENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                      (619)
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    Plasmodium falciparum
                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knobbe Martens Olson & Bear
Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                     (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                 DNA
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                                                                                                                        2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  29,655
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                                                                                                                        Score 36.2; D
Pred. No. 2.2;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                          DB 2;
                                                                                                             53;
                                                                                                                                          Length 4507;
                                                                                                             Indels
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RESULT 11
US-08-281-714-1
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                                                      Sequence 1, Application US/08281714 Patent No. 5658772
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08749522
Patent No. 6096950
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 1034 TTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAAT 1093
                                                                                                                                                                                                     1094 CCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (414) 277-5709
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                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Baker, Jean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE
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                                                                                                                                          TAATATCATATTTAATTTATTTATTATATCATATTCATCTTGCATATAAA 1123
                                                                                                                                                                      TTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAA 1205
                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                            87;
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53202-4497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2781 base pairs
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                                                                                                                                                                                                                                                                                                                            Conservative
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Russell, Sandra
Sauer, Brian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                double.
                           Joan T
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50.6%;
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                                                                                                                                                                                                                                                                                                                                         Score 36; DB 3; Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                        Length 2781;
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                                                                                                                             US-08-484-438-3
                                                                                                                                        RESULT
                                                                                Patent No. 5811098
Patent No. 5811098
                                                                                                              Sequence 3,
                                                                     GENERAL INFORMATION
                             APPLICANT
                                             APPLICANT:
                                                         APPLICAN
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                                                                                   5811098 5780031
                                                                                                              Application US/08484438
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Query Match
Best Local Similarity
Tanhes 76; Conserv
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pair
                 1154 TTAGCACATGCTTAAATATCAAA 1176
                                                                                          1094 CCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTT 1153
                                                                                                                                                           1034 TTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAAT 1093
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Siegell, Barbara C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
302 TATTAACATACATTAACATTGAA
                                                             MEDIUM TYPE: Diskette, MEDIUM TYPE: 1.0 MB
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                nucleic acid
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                  2726 base pairs
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Jennie B.
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                                                                                                                                                                                                         2.8%;
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                                                                                                                                                                                                         Score 35.8; Di
Pred. No. 2.2;
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                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                            67;
                                                                                                                                                                                                                        Length 2726;
                                                                                                                                                                                            Indels
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Culouscou, Jean-Shoyab, Mohammed

Plowman, Gregory D. Culouscou, Jean-Michel

Hellstr m, Ingegerd Siegall, Clay B.

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RESULT 13
US-08-323-170B-1/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                      3302 TGGTATATTTTAATCTAGGCATCACATTGATTTGAGCTATATATTATTTTG 3250
                                                                                                   1220 GAGCACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTTTG 1272
                                                                                                                                             3360 CATGCTTGTCCTAAAATTAACTACATATAGCA--AGATTGGCACATCTTTTGTGGGTA
                                                                                                                                                                              1160 CATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGATGTGCAAGGG
                                                                                                                                                                                                                                                 1100 TACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTTTTAGCA 1159
                                                                                                                                                                                                                                                                                       3480 AATGGTTTTATTAGTTGGAATTGTTTTTTAAAGTTAAGATTTGTTTTAAATAAATTAAGA 3421
                                                                                                                                                                                                                                                                                                                          1040 AAGCTTTAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 5555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Legan-
NAME: Misrock, S. Legan-
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
REFERENCE/TOOK INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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JENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                Conservative
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34..3210
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Pred. No.
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US-08-781-891-207/c : Sequence 207, Application US/08781891 ; Patent No. 6090620

GENERAL INFORMATION:

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Best Local S
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: '29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                               1130 TTCATATCTCAACTAAGATAACTTTT 1155
                                                                   2653
                                                                                                                                     2713
                                                                                                                                                                     1010 TGTATTAGAAGTAAAAGTAGCTTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACT 1069
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2593 TATTTCTTTATTATAAGGTATCATCT 2568
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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LOCATION:
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                                                                   ATTATATACTACAGAATTATTAACTAAGTTACCTAAACTTTTATTTTCTTTATTCCATTT
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California
                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                               Conservative
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SYSTEM: PC-DOS/MS-DOS
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48.1%;
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Pred. No. 8
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Best Local Similarity
Matches 105; Conserv
                                                                                                                      Sequence 2, Application US/07715751B Patent No. 5391725
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INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
                                                                                                      SENERAL INFORMATION:
                                                                                                                                                                                                                         17846 ACCAAGTATATATCTACATACATG 17823
                                                                                                                                                                                                                                                                                          17906 TTTCTATTTAATTTTAGACATAAATAATAGAAGAAAACTACTCCTGAAAGTTGTCCTCTG 17847
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                                                                                  APPLICANT:
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APPLICATION NUMBER: US
FILING DATE: 27-DEC-19
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MEDIUM TYPE: Floppy disk
   TITLE OF
                   FITLE OF INVENTION:
                                                     APPLICANT:
                                                                      APPLICANT:
                                                                                                                                                                                                                                                         348
                                                                                                                                                                                                                                                                                                                                                                                                230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 TATATATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTA 229
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ZIP: 98104-7092
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                                                                                                                                                                                                                                           ATAAAGGATATATCTGGAACTATG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Schellenberg, Gerald D.
INVENTION: GENE AND GENE PRODUCTS RELATED
INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP 6300 Columbia Center,
                                CORUZZI, GLORIA M
EDWARDS, JANICE W
WALKER, ELSBETH L
BREARS, TIMOTHY B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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SYSTEM: PC-DOS/MS-DOS
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SEQUENCES
                NOVEL ORGAN-SPECIFIC PLANT PROMOTER
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Pred. No. 14;
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Best Local Similarity
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                                                                                                                             1517
                                                                                                                                                                                                                           1061 CATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACTCAGAATGTTATCCCATCT 1120
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                                                                                                                                                                                                                                                                                            1001 TCATCTGGATGTATTAGAAGTAAAAGTAGCTATCCAAAGCTTTAAATTTGTAGAACT 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090 TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                            1241 GTTACCATATGTTAGGAAATAAAATTATTTTGC 1273
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ADDRESSEE: PENNIE &
STREET: 1155 AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MISROCK, S. L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TTTATATTTTGATTCAAAATAATTTTATTTAGC 1365
                                                             TTGTCATTTGGAAGTCACTTGTGAATAGATGTGCAAGGGGAGCACATATTGGATGTATAT 1240
                                                                                                                             AAAGCATTTTTCATATCTCAACTAAGATAACTTTTTAGCACATGCTTAAATATCAAAGCAG 1180
                                                                                                                                                                                             AATCTAATGAGAATAATTTGCGGTGTAGATATGATTCTGTCTTATAGATAAATGATATTT 1518
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Pred. No. 4;
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Search completed: March 29, Job time: 3554 sec 2002, 19:53:01

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Result
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Maximum DB seq length: 20
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## ALIGNMENTS

AL525341 978 bp mRNA EST 13-FEB-2001 AL525341 LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CS0DC011YC02 prime, mRNA sequence. AL525341

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RESULT AL525341 LOCUS

ACCESSION DEFINITION

AL525341.1 GI:12788834

REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS SOURCE ORGANISM FEATURES COMMENT source Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope EST BP 191 91006 EVRY cedex - Francemail: segref@genoscope.cns.fr, Genoscope - Centre National de Sequencage Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. W.B., Gruber, C., Jessee, J. and Polayes, D. (bases 1 to 978) 91006 EVRY cedex - France /tissue\_type="neuroblastoma cells"
/lab\_host="DH10B"
/lab\_host="DH10B"
/note="0'organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="0'organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6 by Life Technologies. /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="CSODC011YC02" /ector 'sex="male" clone\_lib="LTI\_NFL003\_NBC3" ocation/Qualifiers Web : www.genoscope.cns.fr Contact : Feng Liang Life Library was

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                                                                                                              AATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATT 519
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segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                  cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.
                                                                                                                                                                                                                                                                                                                                                               http://fulllength.invitrogen.com"
212 c 162 g 322 t 2
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2 (bases 1 to 1293)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNa libraries for rapid discovery of new Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                 Mammalia; Eutheria; Rodentia; Survey, Mammalia; Eutheria; Rodentia; Survey, 1 (bases 1 to 1293)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
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A, clone_lib:RIKEN full-length enriched mouse cDNA library
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GTGCGGGCTGGTGGCTGTGGCAGCGGCGGCGGCAGGACTCCGGCACTATGAGCGGCTT

Query Match Best Local

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Similarity 82.4 24; Conservative

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/db_xref="GI:12842843"
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GTAGTTGAAGTACCACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTA 286
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Location/Qualifiers
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BP 191 91006 EVRY cedex - FI
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                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and Eco RV sites of the pCMVSPORT 6 cloned into the Not I and Eco RV sites of the pCMVSPORT 6 rector. Library is not normalized, but is the control for vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a rechnologies of the pCMVslile division of Invitrogen 9800 Medical Center Drive Rockville
                                                                                                                                                                                                                                                                                                                                        fliangelifetech.com URL:
http://fulllength.invitrogen.com"
http://fulllength.invitrogen.com"
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/ob_xref="taxon:9606"
/clone="CSODA012YD02"
/clone_lib="LTI_NFL011_NBC1"
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Primates;
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1; Mismatches 1;
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                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informatior
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10598 row: n column: 10
High quality sequence stop: 837
Location/Qualifiers
11.932
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, )
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602622839F1 NCI_CGAP_Skn4
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  /organism="Homo sapiens"
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/clone_lib="NCI_CGAP_Skn4"
/clone_lib="NCI_CGAP_Skn4"
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/lib_host="DH10B_(T1_phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo of Site_2: SalI; Cloned unidirectionally. Promer: Oligo of Site_2: Note: this is a NCI_CGAP_Library."

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BP 191 91006 EVRY cedex - France
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)3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA-was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://fulllength.invitrogen.com"
146 c 193 g 218 t
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/clone_lib="LTI_NFL006_PL2"
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BG674343
BG674343.1 GI:13905739
EST.
                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs - femail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) E
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) E
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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National Institutes of Health,
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Mammalia; Eutheria; Primates;
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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                                                        /clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6;
                                                                                                    /clone="IMAGE:4745743"
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/db_xref="taxon:9606"
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                                GTGTTCATCTGGATGTATTAGAAGTAAAAGTAGTAGCTTT
                                                                                              GTTCCATCACCAGAAAAACTAATGAGATTTCTCTGGAATACAAGCTGATATTGCTACATC
                                                                                                                                               GGATGCTTTACCACCACCCTGTGAATCTGCCTGCACAGTACCAACAGACGTGGATAAGTG
                                                                                                                                                                                                          GAATACAACTTTGTCTGAGAGCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGT
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    GGAGTTTGAAGTAAGTGAGTTTGAAATTATTTGTAACTTT
                                                                 GTCCATAACAGAAAAGTAATGAAATTCTTGGGATACAGATGAATATGAAATGGGTCAACT
                                                                                                                             GGATGCTTAACAGCAGCC -- TTGAATCTGCCTGGAAAGTACCAACAGAAGTAGATAAGGG
                                                                                                                                                                                                                                                       TCATGACCATGGAAAGCATTAGTGACTAAGAAAACGAATGGACAACGGAATCAGTTGCAT
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hes 766;
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                                                                                                                                                                                                                                                      GCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTC
                                                                 AGATTGCTACAAAGGACCCTTTAAACCCTATTAAACAGAGATGTGAAAAAAAGGAAAACTTC
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1 (bases 1 to 773)

NHH-MGC http://mgc.nci.nih aav/
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                     Similarity
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Plate: LLAM10685 row: n column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Miklos Palkovits, cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE: 4798285"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="hypothalamus"
/lab_host="DH10B"
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_96 Homo sapiens cDNA clone IMAGE:4798285
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Pred. No. 3.6e-171;
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244 GCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTC

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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                           e: LLAM11264 row: e column: quality sequence stop: 749.
                                                                                                                                                                                                                                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.4 kb. Library prepared by Life
                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:5109100"
/clone_lib="NIH_MGC_12"
                                                            /tissue_type="cervical carcinoma/
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                   organism="Homo sapiens"
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VERSION KEYWORDS

ORGANISM

Homo

sapiens

Eukaryota; nman.

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

ACCESSION DEFINITION

mRNA sequence. BG713976 BG713976.1 GI: EST.

LOCUS

BG713976 772 bp 602674374F1 NIH\_MGC\_96

Homo

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08-MAY-2001 IMAGE:4796875

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TGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAGAC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM10682 row: c column:
High quality sequence stop: 767.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

146 c 197 g 194 t
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/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
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BI259308
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Plate: LLAM11271 row: 1 column: 12
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection
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Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submission
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Fax:81-45-503-9216)
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/clone_lib="RIKEN full-length enriched mouse
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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/clone="InAGE:4705253"
/clone_lib="NIH_MGC_87"
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/lab_host="DH10B (phage-resistant)"
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BASE COUNT ORIGIN

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Query Match Best Local 9

Local Similarity

56.5%; 94.1%;

Score 721; DB 11; Pred. No. 8.1e-166; Pred. No. 8.1e-36;

Length 915; Indels

18;

Matches

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Conservative

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601 629 541 569 481 509 421 449 361

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121 CTCAAAAATGAGAAAGGACAATATATATCTCCATTTCATGATATTCCAATTTATGCAGAT
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                                                                               AAAAGGAATCAGTTGCATGAAT---ACAACTTTGTCTGAGAGCCCCTTCAAGT-GTGATCC
                                                                                                                            ATTCAAAAGCACTCATGACCA-TGGAAAGCATTAGTGACTTAAGAAGAACGCATTGGAAC
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Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
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   CATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCÀCGC
                                                                                                                                                                                                                   BG708966 845 bp mRNA EST 07-MAY-2001
602675112F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797723
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BG708966.1
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National Institutes of Health, Mammalian
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plate: LLAM10684 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall'XNOI (gtcg pBluescript KS+); Site_1: BamHI; Site_2: Sall'XNOI (gtcg primed using primer 5 'TTTTTTTTTTTTVN-3'); Oligo-dT primed using primer 5 'TTTTTTTTTTTTTTTTVN-3'); Oligo-dT primed using primer 5 'TTTTTTTTTTTTTTTN-3'; Size primer 5 'TTTTTTTTTTTTTN-3'; Size primer 5 'Notation and constructed using the constructed using the constructed by M. Brownstein (NIMH/NHGRI, National constructed by M. Brownstein (NIMH/NHGRI, National constructed by M. Brownstein (NIMH/NHGRI, National constructed by M. Brownstein (NIMH/NHGRI)
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/lab_host="DH10B"
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BG721093.1
EST.
                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., E
CDNA Library Preparation: Michael J. Brownst
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Cons
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution if
found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 762)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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## ALIGNMENTS

ACCESSION VERSION KEYWORDS

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AL519324

prime, mRNA sequence.

RESULT AL519324 LOCUS

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DEFINITION

AL519324 826 bp r AL519324 LTI\_NFL011\_NBC1

mRNA

nRNA EST 13-FEB-2001 Homo sapiens cDNA clone CSODA012YD02

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REFERENCE AUTHORS FEATURES COMMENT SOURCE TITLE JOURNAL ORGANISM source Contact: Genoscope Genoscope • Centre National de Sequencage BP 191 91006 EVRY cedex • France Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Homo sapiens Email: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; l (bases 1 to 826) naman. segref@genoscope.cns.fr, /tissue\_type="neuroblastoma cells"
/lab\_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for the normalized libraries. Library /sex="male" /clone\_lib="LTI\_NFL011\_NBC1" /clone="CS0DA012YD02" /organism="Homo sapiens" /db\_xref="taxon:9606" ocation/Qualifiers Web : www.genoscope.cns.fr. constructed ρy Life

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                                                                                                                           TCAAGTGTGATCCTGATGCTGCCAGAGCCAT
                                                                                                                                                                                CTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCT
                                                                                                                                                                                                         CTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCT
                                                                                                                                                                                                                                   TCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                CCGACTGGAAAGTCATTGCCATTAATGTGGATGATCCTGATGCAGCCAATTATAATGATA
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153 c 203 g 212 t Lothers
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10707 row: h column: 05
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Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
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08-MAY-2001
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cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://mgc.nci.nih.gov/";
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                                                          CTCTCCTTGTCAGTCGGCGCGCGCGTGCGGGCTGGTGGCTCTGTGGCAGCGGCGGCGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                       M. Brownstein (NIMH/NHGRĪ, Nations Note: this is a NIH_MGC Library." /organism="Homo sapiens" /clone="IMAGE:4813492" /clone="IMAGE:4813492" /clone_lib="NIH_MGC_95" /tissue_type="hippocampus" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xrer=-taxu...../
/note="forgan: brain; Vector: pBluescriptk (modilized /note="forgan: brain; Vector: pBluescript kS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag /pBluescript kS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag /pBluescript kS+); Sit
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                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 771)
                                                                                                                                                                               e: LLAM11264 row: e column: 05 quality sequence stop: 749.
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.4 kb. Library prepared by Life
                                                  /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                /clone="IMAGE:5109100".
/clone_lib="NIH_MGC_12"
                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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BG715195
BG715195.1 GI:
                                                            Homo sapiens
                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10685 row: n column: 14
High quality sequence stop: 773.
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cDNA_Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:4798285"
/clone_lib="NIH_MGC_96"
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/lab_host="DH10B"
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1 (bases 1 to 905)
NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, N
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602294777F1 NIH_MGC_86 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/lab_host="DHIOB (phage_resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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National Institutes of Health, M
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
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602596421F1 NIH_MGC_87
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Location/Qualifiers
        /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="organ: breast; Vector: pcNv-SPORT6; Site_1:
Site_2: SalI; Cloned unidirectionally; oligo-d7 pri
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full-length clones and constructed by Life Technolo
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:4705253"
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                                                          Email: cgapbs:r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                        mRNA sequence:
BE887465
                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                   BE887465 628 bp
601508111F1 NIH_MGC_71
                                                                                        Contact: Robert Strausberg,
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                       BE887465.1
                                                                                                   Unpublished (1999)
                                                                                                                                                                                             Homo sapiens
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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IMAGE:3909506
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AW009649 660 bp.; mrnA EST 08-MAR-2000 ws85e03.x1 NCI_CGAP_CO3 Homo sapiens cDNA clone IMAGE:2504764 3' similar to SW:IPYR_BOVIN P37980 INORGANIC PYROPHOSPHATASE;, mRN
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plate: LLAM9723 row: f column: 03
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPOF
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High quality sequence store
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Elias Campo, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Ist strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization.
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co3"
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10682 row: c column: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG713976 772 bp mRNA EST 08-MAY-2001 602674374F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4796875
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Location/Qualifiers
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                    235
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                    a
                                                                                               /note-*Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the
                  Cap-trapper method (Carninci, in preparation). Li
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Lib
1 146 c 197 g 194 t
                                                                                                                                                                                                                                    /tissue_type="hypothalamus"
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                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 955)
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                                                                                                                                                                                                                                                                                                     BF791373 955 bp
602251332F1 NIH_MGC_84
DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                    Contact: Robert Strausberg,
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                BF791373.1
                                                                                                                                                                                                                                                                                         mRNA sequence
                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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mRNA
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High quality sec
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/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="pH10B (phage-resistant)"
/note="organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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/db_xref="taxon:9606"
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Pred. No. 2e-302;
               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599;
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; vector: pDNR-LIB (Glontech); Site_1:
/note="Organ: testis; vector: pDNR-LIB (Glontech); Site_2: SfiI (ggccattatggcc);
/note="Organ: testis; vector: pDNR-LIB (ggccattatggcc);
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Best Local Similarity
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National Institutes of Health, M
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Plate: LLAM10570 row: p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                    190
                                                                                                                                    Conservative
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                                                                                                                                                                                                                                /clone="IMACE:4705016"
/clone_lib="NIH_MGC_87"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Organ: breast; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10040 row: f column: 02
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1. (bases 1 to 998)
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                                                                                                                                                        High quality sequence start: 52
High quality sequence stop: 761
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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National Institutes of Health, M
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4375297"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                                /tissue_type="hippocampus"
/lab_host="DH10B"
                                                                     /clone_lib="NIH_MGC_95"
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                                                                                                                             mRNA sequence.
BG676397
BG676397.1 GI:
EST.
 Contact: Robert Strausberg,
                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 932)
                                                                                                                                                                                 BG676397 932 bp mRNA
602622839F1 NCI_CGAP_Skn4 Homo
                Unpublished (1999
                            NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                 Homo sapiens
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706; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
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Plate: LLAM10598 row: n
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/lab_host="DH10B (T1 phage-resistant)"
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (
Average insert size 1.5kb. Library constructed by Lii
Technologies. Note: this is a NCI_CGAP Library."
155 c 208 g 260 t
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                  TGCATGAATACAACTTTGTCTGAGAGGCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCC
TGCATGAATACAACTTTGTCTGAGAGCCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCC
                                                                                                                                                              AATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACTTTGCCATTGATATTATTAAA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at14f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355119 3' similar to SW:IPYR_BOVIN P37980 INORGANIC PYROPHOSPHATASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 448.
.Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White,Y., Wylie,T., Watersto
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                             Barstead.
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/db_xref="taxon:9606"
/clone="IMAGE:2355119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'dev_stage="adult, age 64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone_lib="Barstead aorta HPLRB6'
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s; Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                 99 g
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Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM10593 row: a column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) D Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                314
                   /db_xref="taxon:9666"
/clone="IMAGE:4745743"
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/clone="InAGE:4745743"
/clone="Nort="NORTHIDE (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1:
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1:
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Query Match

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Score 581;

DB 11;

Length 996;

Matches

Conservative

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Pred. No. 5.4e-289; Mismatches 0;

Indels

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Gaps

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Best Local Similarity

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                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 882)
             High quality
                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution i found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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602286503F1 NIH_MGC_95 Homo sapiens cDNA
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RESULT 18 BG777143

DEFINITION

BG777143 711 bp 602664359F1 NIH\_MGC\_59

Homo

sapiens

CDNA EST clone

15-MAY-2001 IMAGE:4809591

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LOCUS

VERSION ACCESSION

KEYWORDS

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GI:14047460

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/lab_host="DH10B"
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/clone_lib="NIH_MGC_95"
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Tissue Procurement: ATCC
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/lab_host="DH10B (T1 phage resistant)"
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NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D., cDNA_Libzary Preparation: Life Technologies, Inc. cDNA_Libzary Arrayed by: Christa Prange, Th. I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                    cgapbs-r@mail.nih.gov
pBluescript [KS+); Site_1:
                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4817474"
                   /note="Organ:
                                    /tissue_type="hippocampus"
/lab_host="DH10B"
                                                                        /clone_lib="NIH_MGC_95"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:13974812
                   brain; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens cDNA clone IMAGE: 4817474 5'
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or: pBluescriptR (modified BamHI; Site_2: SalI-XhoI
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                                                                                                                                                                                                                                                                                                                                                                           17 CTCTCCTTGTCAGTCGGCGCCGCGTGCGGGCTGGTGGCTCTGTGGCAGCGGCGGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                        AAACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCC
                                                                                                                                                                                                     AAAATGGAGATTGCTACAAAGGACCCTTTAAACCCTATTAAACAAGATGTGAAAAAAGGA
                                                                                                                                                                                                                                         ATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCTAATGCA
                                                                                                                                                                                                                                                                                                                                              ATTGCCATTAATGTGGATGATCCTGATGCAGC 588
                                                 GGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTC
                                                                               AATGACCCAATTGATGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATT
                                                                                                                      ATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGGCTGTTGTGGTGAC
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                                        GGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTC
                                                                                                  AATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATT
                                                                                                                                         ATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGGCTGTTGTGGTGAC
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Pred. No.
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BG702317
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COMMENT
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                                                                                                       AUTHORS
TITLE
                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 769)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG702317 769 bp
602683563F1 NIH_MGC_
Unpublished (1999)
Contact: Robert St
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BG702317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-2001
IMAGE:4816311
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BASE COUNT
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Best Local Similarity 100.0%;
Matches 570; Conservative
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GCTGAAACCTGGCTACTTAGAAGCTACTGT 648
                                                                      TGCCATTAATGTGGATGATCCTGATGCAGCCAATTATAATGATATCAATGATGATGTCAAACG
                                                                                                                                            CGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGGAAAGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                              ACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATGCAGATAAGGATGTGTTCACATGGTAGTTGAAGTACCACGCTGGTCTAATGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGAGTCTTCCTCAAAAATGAGAAAGGACAATATATCTCCATTTCATGATATTCCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Proparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Michael J
Toshiyuki and Piero Carninci (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Lil 140 c 201,g 194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4816311"
/clone_lib="NIH_MGC_95"
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/lab_host="DH10B"
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Pred. No. 2.6e-283;
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TCTGGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCCAGGGCACAATGATAAACATA 419
                                                                      AAGATGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCCCCGTATAAAGGATATA 359
                                                                                                          CACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAAACCCTATTAAAC
                                                                                                                                          CACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAAAACCCTATTAAAC 299
                                                                                                                                                                             CATTTCATGATATTCCAATTTATGCAGATAAGGATGTTTTCACATGGTAGTTGAAGTAC
                                                                                                                                                                                                                                              GGCAGCGGCGGCGGCAGGACTCCGGCACTATGAGCGGCTTCAGCACCGAGGAGCGCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                        567;
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602331122F1 NIH_MGC_91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
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/rhores of Health, Mammalian Gene Collection (MGC)
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RC1-CN0008-290300-014-d09 CN0008
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                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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300-014-d09&t3=2000-03-29&t4=1)
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                                                               /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
          tissue mRNA and cDNA amplification
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                                                                                                                                                                        /dev_stage="Adult"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC). Uppublished (1999)
                             found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM10183 row: o column: 14
                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG179769
High quality sequence stop: 667
Location/Qualifiers
                                                                                                                                               Tissue Procurement: DCTD/DTP
                                                                                                                                                                             Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    BG179769 1076 bp
602328856F1 NIH_MGC_91
                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                     BG179769.1
                                                                            CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 9e-282;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562;
                                                    sequence.
AW873109
AW873109.1
                                                                                         AW873109 585 bp m
hq22h11.x1 NCI_CGAP_Adr1
similar to SW:IPYR_BOVIN
             Homo sapiens
                                         EST
Eukaryota; Metazoa;
                             numan.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not
Site_2: Sali; Cloned unidirectionall; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4430437"
/clone_lib="NIH_MGC_91"
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100.0%;
Chordata; Craniata;
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Pred. No. 3.6e-279;
                                                                                                                       mRNA
                                                                                           Homo sapiens cDNA clone IMAGE:3120165 3' P37980 INORGANIC PYROPHOSPHATASE;, mRNA
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Vertebrata; Euteleostomi;
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719 AAAGATAAGGACTTTGCCATTGATATTAATTAAAAGCACTCATGACCATTGGAAAGCATTA 778
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TTGTGAATAGATGTGCAAGGGGAGCACATATTGGATGTATATGTTACCATATGTTAGGAA
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                                                                             CAACTAAGATAACTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCAC
                                                                                                                                                                                                                                TCTGCTGTGACTAATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCT 1138
                                                                                                                                                                                                                                                                                 Possible reversed clone: polyT not
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emmert-Buck, M.D., Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Email: cgapbs remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL, info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: adrenal gland; Vector: pcMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.2 kb. Library
constructed by Life Technologies. "
constructed by Life Technologies. "
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/clone="IMAGE:3120165"
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National Cancer Institute, Cancer Genome Anatomy Project
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmert-Buck, M.D., Ph.D.
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signet ring cell features"
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Query Match Best Local S Matches 552

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National Institutes of Health, Mammalian
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High quality sequence stop: 592.
Location/Qualifiers
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                    /tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
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                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:3846924"
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                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BG721093
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602692932F1 NIH_MGC_97
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                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                          http://image.llnl.gov
Plate: LLAM10737 row:
                                                                                                        found through the I.M.A.G.E. Consortium/LINL at:
                                                            quality sequence stop:
/organism="Homo sapiens'
/db_xref="taxon:9606"
                                          Location/Qualifiers
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                                                                         AA694204 639 bp mRNA EST
zi42c12.sl Soares_fetal_liver_spleen_INFLS_S1 F
clone IMAGE:433462 3' similar to SW:IPYR_BOVIN
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                                                              PYROPHOSPHATASE ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4825206"
/clone_lib="NIH_MGC_97"
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                                GI:2695142
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Pred. No. 6.9e-270;
0; Mismatches 1;
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ORGANISM

Homo sapiens

human.

Eukaryota;

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
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                                    TGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGTAGCTTTTCAAA
                                                       TGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGTAGCTTTTCAAA 1041
                                                                                                     AGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCTGGAATACAAGC
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WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 639)
Hillier,L., Allen,M., Bowles,L.,
Krizman,D., Kucaba,T., Lacy,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.linl.gov) for fu
possible reversed clone: similarity on wrong
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University/School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:433462"
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 2.2e-269;
D; Mismatches 1;
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οy

735 CCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGA 794

Matches

541;

Conservative

Similarity

2.4e-268

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RESULT 30
AA493425/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Seg primer: -40ml3 fwd. ET from An
High quality sequence stop: 416.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was with a Not I - oligo(dT) primer. Double-stranded with Not ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of
                                                                                                                   modified pT7T3 vector. Library went
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                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                        /tissue_type="colon"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                           /sex="pooled"
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NCI_CGAP_CO3 Homo sapiens cDNA clone IMAGE:900629 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D
CDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                 Unpublished (1999)
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National Institutes of Health, Mammalian
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Plate: LLAM10724 row: g column:
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
Cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                    quality sequence stop: 744.
/organism="Homo sapiens"
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/clone="IMAGE:4820008"
/clone_lib="NIH_MGC_95"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for 'full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 139 c 195 g 191 t lothers
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; Pred. No. 2.7e-267;
0; Mismatches 0;
                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae;
                               Mammalian
                                                                                                                                                                                                  CDNA
                                                                                                                                                                                                  clone
                               Gene
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                                                                           Hominidae;
                               Collection (MGC)
                                                                                                                                                                                                  08-MAY-2001
IMAGE:4792790
                                                                                         Euteleostomi;
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COMMENT

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558 TTGCCATTAATGTGGATGATCCTGATGCAGCCAATTATAATGATAT
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Local Similarity 99.8%;
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                                                                                                                                                                                                       TCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGGCTGTTGTGGTGACA
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                                                                                                                        ATGACCCAATTGATGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAM10671 row: i column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="hypothalamus"
/lab_host="DH10B"
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/clone_lib="NIH_MGC_96"
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Pred. No. 3e-265;
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Best Local S
Matches 582
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                                                                                                                                                                                                                                                   61
                                                                                                                                   GAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGG
                                                                                                                                                                                  TGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTG
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                                                                                                                                                                                                                                                                                                                  TCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACG
               AGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAAC
                                                CTGTTGTGGTGACAATGACCCAATTTATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAG
                                                                       CTGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAG
                                                                                                                   GAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGG
Plate: LLAM9598 row: o column: High quality sequence stop: 611.
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601457932F1 NIH_MGC_66 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
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/tissue_type="adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.8%;
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Pred. No. 1.1e-263;
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TITLE
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            TAAAAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGAATGGAAAAGGAAT 807
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TAAAAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGAATGGAAAAGGAAT
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                Seq p
High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                primer: -40UP from Gibco
                                                                                                                                                                     188
                                                                41.4%;
llarity 100.0%;
Conservative
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                                                                                                                                                              /note="Organ: lymph node; Vector: pCMV-SPORT6; SalI; Site_2: NotI; Cloned unidirectionally. F Oligo dT. Average insert size 1.25 kb. Life Tecatalog #: 11547-015"

a 123 c 102 g 217 t 1 others
                                                                                                                                                                                                                                                                              /clone="IMAGE:2850091"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, fol
cell"
                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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SW:IPYR_BOVIN P37980
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Lym12 Homo sapiens cDNA clone IMAGE:2850091 3'
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Pred. No. 1.3e-261;
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similar to
                                                                                                                                      Seq primer: -40UP from Gibco
                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1001 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D.
              /clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                          /clone="IMAGE:1883873"
                                                                                                                        Location/Qualifiers
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NCI_CGAP_Lu5 Homo
SW:IPYR_BOVIN P379
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lung; Vector: pT7T3D-Pac (Pharmacia)
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980 INORGANIC PYROPHOSPHATASE
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                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523;
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome
351 Guo Shoujing Road, Zhangji
                                                                                                                                                                                                                                                                                          AV706813
AV706813
                                                                                                        Zeng,L.,
                                                                                                                                                                                         Eukaryota; Metazoa;
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(bases 1 to 690)
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                                                                                        ,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Che,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Hu,R., Chen,J., Chen,Z. and Han,Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinold, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia)_digested with Not I and
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Eukaryota;
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                                                                     mRNA sequence.
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602326583F1 NIH_MGC_91
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clone is available
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/db_xref="taxon:9606"
/clone="ADBCOF06"
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/dev_stage="Adult"
/lab_host="SOLR"
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AGTAAATTCTGCTGTGACTAATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTT
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                                                                                                                     AAACTAATGAGATTTCTCTGGAATACAAGCTGATATTGCTACATCGTGTTCATCTGGATG
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Plate: LLAM10177 row: f column:
High quality sequence stop: 759.
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National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
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Clone distribution: MGC clone distribution information can
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/lab_host="hH10B (phage-resistant)"
/note="Organ: prostate; Vector: pcMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NHH_MGC Library."

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/db_xref="taxon:9606"
/clone="IMAGE:4427925"
/clone_lib="NIH_MGC_91"
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DEFINITION 601159361T1 NIH_MGC_53
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                                                                                                                                                                                 AGAAGGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTT 718
                                                                                                                                                                                                                                                                                                                             GATATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTT 658
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AAAGATAAGGACTTTGCCATTGATATTAAAAAGCACTCATGACCATTGGAAAGCATTA
                                                                    AAAGATAAGGACTTTGCCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGCATTA 778
                                                                                                                                               AGAAGGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTT
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High quality sequence stop: 760.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Glortech);
Site_1: Sfil (ggccgctctggcc); Site_2: Sfil (ggccattatggcc);
Duble-stranded cDNA was prepared from cell line RNA.
5; and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5; -CACGGCCATTATCGCC-3; and 3; adaptor sequence: 5; -CACGGCCATTATCGCC-3; Adaptor sequence: 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length clones and was constructed Laboratories (Palo Alto, CA)."
177 c 145 g 265 t
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/db_xref="taxon:9606"
/clone="IMAGE:351099"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 515; DB 10;
Pred. No. 6.8e-255;
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National Cancer Institute, Cancer Genome Anai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                 round through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Michael J. Brownstein, Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                     Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can b
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modified pT7T3 vector. Lib
constructed by Bento Soares
                               a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Long RI sites of the I and cloned into the Not I and Eco RI sites of the
                                                                                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with
                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2418052"
                                                                                                                                                                                 /clone_lib="NCI_CGAP_Pr22"
/sex="male"
                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                          'lab_host="DH10B"
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                                                                                                                                                                tissue_type="normal prostate"
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M. Fatima Bona
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602369062F1
                                                                                                                                   1 (bases 1 to 940)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                            mRNA sequence
BG254456
                                                                         Tissue Procurement: DCTD/DTP
                                                                                      Email: cgapbs-remail.nih.gov
                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                    Unpublished (1999)
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           Homo sapiens
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found through the
            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
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NIH_MGC_91
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Pred. No. 2.5e-252;
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Best Local
                              ORGANISM
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                                                                     mRNA sequence.
BE887538
BE887538.1 GI:
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                           EST
                                                                                                             BE887538 503 bp
601508191F1 NIH_MGC_71
                                            numan
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Plate: LLAM10305 row: 1 column:
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: prostate; Vector: pcMV-SPORT6; Site_1: Not
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NHL_MGC Library."
a 183 c 232 g 250 t
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/clone_lib="NIH_MGC_91"
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/db_xref="taxon:9606"
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 Chordata;
Primates;
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Pred. No. 3.3e-249;
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  Craniata; Vo
Catarrhini;
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               Vertebrata; Euteleostomi;
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  Hominidae;
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IMAGE:3909526
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                                                                                                AAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACT
                                                                                                                                                                                              ATGGTGCCATCCCTCAGACTTGGGAAGACCCCAGGGCACAATGATAAACATACTGGCTGTT
                                                                                                                                                                                                                               ATGGTGCCATCCCTCAGACTTGGGAAGACCCCAGGGCACAATGATAAACATACTGGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503;
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Location/Qualifiers
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Plate: LLAM9723 row:
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 503)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6;
Site_2: Sali; Cloned unidirectionally. Pri
Average insert size 2.1 kb. "
97 c 126 g 126 t
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/clone="IMAGE:3909526"
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lmer: Oligo dT.
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                                                                                                                                             773 GCATTAGTGACTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCT 832
                                                                                                                                                                                                                                                                                                                                                            455 GAGAGCCCCTTCAAGTGTGATCCTGATGCTGCAGAGCCATTGTGGATGCTTTACCACCA
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similar to
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
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1 (bases 1 to 585)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: NCI-CGAP clone distribution
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="moderately-differentiated adenocarcinoma"
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TATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCTAATGCAAAA 60
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                                                                                             623;
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BG777846
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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Plate: LLCM1651 row: d column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                             Conservative
                                                                                                                                                                                                                              Library."
                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="adenocarcinoma"
/lab_host="hH10B (T1 phage-resistant)"
/lab_host="hH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA);
Double-stranded cDNA was prepared from cell line RNA);
Site_1: Adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGACATG-dT(30)BN-3'
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                                                                                                                                                                                                                                                                                                 (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
                                                                                                                                                                                                                                                                              Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="NIH_MGC_60"
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                                                              http://image.llnl.gov
Plate: LLAM11263 row: p column:
High quality sequence stop: 737.
Location/Qualifiers
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Tissue Procurement: ATCC
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BI260339
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602969372F1 NIH_MGC_12
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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         /db_xref="taxon:9606"
/clone="IMAGE:5108993"
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wn88b03.x1
similar to
                                                                                                                                                                                sequence.
AI922084
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat
                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 624)
                                                                                                                    Homo sapiens
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Pred. No. 1.1e-248;
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V P37980 INORGANIC
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                                            Anatomy Project (CGAP)
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Tissue Procurement: Christopl
Emmert-Buck, M.D., Ph.D.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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Hawkins, P.R. and Hillman, J.L.
Human pyrophosphatase
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Post-processing: Listing first 45 summaries

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Searched:

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human.
Homo sapiens
Eukaryota; Me
                                                                 Homo sapiens,
IMAGE:3345496,
                                             BC001022
BC001022.1
                                                                                           BC001022
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                             GI:12654394
                                                                 1301 bp mRNA pyrophosphatase, mRNA, complete
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                                                                    cds
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GGGGCTCTCTCCTTGTCAGTCGGCGCCGCGTGCGGGCTGGTGGCTCTGTGGCAGCGGCGG
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                                                                             CGGCAGGACTCCGGCACTATGAGCGGCTTCAGCACCGAGGAGCGCGCCGCGCCCCTTCTCC
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Series: IRAL Plate: 5 Row: n Column: 19
This clone was selected for fail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,F
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Cgapbs remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Tissue Procurement: Louis M. Staudt, M.D.,
DNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Cor
DNA Sequencing by: National Institutes of Bequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            passed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg, R
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                                                                                                                                                                                                                                                                                                                                                        416
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                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               HMVVEVPRWSNAKMEIATKDPLNPIKQDVKKGKLRYVANLFPYKGYIWNYGAIPQTWE
DPGHNDKHTGCCGDNDPIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAIN
VDDPDAANYNDINDVKRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAID
                                                                                                                                                                                                                                                                                                                                                                        PTDVDKWFHHQKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="pyrophosphatase
/protein_id="AAH01022.1"
/db_xref="GI:12654395"
                                                                                                                                                                                                                                                                                                                                                                                               IIKSTHDHWKALYTKKTNGKGISCMNTTLSESPFKCDPDAARAIVDALPPPCESACTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Lymph, Burkitt lymphoma"
/clone_lib="NIH_MGC_8"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="MGC:1221 IMAGE:3345496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="LocusID:5464"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSGFSTEERAAPFSLEYRVFLKNEKGOYISPFHDIPIYADKDVF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pors7"
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Pred. No. 0;
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              GTGCAAGGGGAGCACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTT.
                                                               CTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGAT
                                                                             CTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGAT
                                                                                                                                            AATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAA
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GTGCAAGGGGAGCACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTT
                                                                                                                              AATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAA
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                                              ATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGG
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AX015063
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2 (bases 1 to 1282)
Huang,C., Zhang,C., Wu,T., E
Li,Y., Han,Z., Wang,Y., Cher
Direct Submission
Submitted (12-JAN-1999) Chir
Shanghai, Guo Shoujing Rd. 3
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product="inorganic pyrophosphatase"
/protein_id="AxP17222.1"
/db_xref="GI:6563256"
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/db_xref="taxon:9606"
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                                                                                                                                               Submitted (26-APR-1999) to the DDBJ/EMBL/GenBank databases. Toshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group; Anagawa 4-9-1, Inage-ku, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp, Tel:81-43-206-3135,
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31. .900
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                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                   Submitted (16-DEC-1999) Clinical Virology, Karolinska Institute, Huddinge University Hospital, Stockholm S-14186, Sweden Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Kanni,L., Johansson,M. and Karlsson,A. Cloning of a human inorganic pyrophosp Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens inorganic pyrophosphatase 1 (PPA1) mRNA, complete cds. AF217186
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VDDPDAANYNDINDVKRLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKDKDFAID
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               PTDVDKWFHHQKN"
                               I I KSTHDHWKALVTKKTNGKG I SCMNTTLSESPFKCDPDAARA I VDALPPPCESACTV
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CCGAGTCTTCCTCAAAAATGAGAAAGGACAATATATCTCCATTTCATGATATTCCAAT 198
                    CTCCGGCACTATGAGCGGCTTCAGCACCGAGGAGCGCGCCCCCTCCTCCCCTGGAGTA 138
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Fairchild, T.A. and Patejunas, G.
Cloning and expression profile of human inorganic Biochim. Biophys. Acta 1447 (2-3), 133-136 (1999)
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Northwestern Healthcare
Evanston, IL 60201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-MAY-1999)
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                                                                                                                                                   /translation="MGGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKDVF
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                                                                                                                                                                                                                                                                                                              tissue_type="heart"
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2650 Ridge A
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1200)
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarsky,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid sequences from prostate tumour tissue Patent: WO 9946374-A 3 16-SEP-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE);
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	17 GGGCTCTCCCTTGTCAGTCGGCGCCGCGGCGGGCGGGCGG	11 GGGGCTCTCTCCTTGTCAGTCGGCGCCGCGCGGGGGGGGG	of 1.8%; Score 788; DB 6; Length 856; zal Similarity 100.0%; Pred. No. 0; 788; Conservative 0; Mismatches 0; Indels 0;	/organism="Homo sapiens" /db_xref="taxon:9606" COUNT 251 a 163 c 222 g 220	SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER (DE); PILARSKY CHRISTIAN (DE) LOCATION/QUALIFIERS  SOURCE 1. 856	UTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. an Pilarsky,C. ITLE Human nucleic acid sequences from ovarian tumour tissue OURNAL Patent: WO 9953040-A 52 21-OCT-1999:	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. EFERENCE 1 (bases 1 to 856)	DS human.	ON AX014862.1 GI:10041129	r 10 862 AX014862 856 bp DNA TTTON Sequence 52 from Patent WO9953040	1131 TAAGATAACTTTTAGCACATGCTTAAATATCAAAG 116	· 1143 TAAGATAACTTTTAGCACATGCTTAAATATCAAAG	1071 CTGTGACTAATCCAAFATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAAC 1	1083 CTGTGACTAATCCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAAC	1011 AAAGTAGTAGCTTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAA	1023 AAAGTAGTAGCTTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAA	963 ATTTCTCTGGAATACAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTA 1	891 CTGCCTGCACAGTACCAACAGGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAG 9	903 CTGCCTGCACAGTACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAG	831 TCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCCTGTGAAT	843 TCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCCTGTGAAT	771 CTAAGAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCT	783 CTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCT 8	711 ATAAGGACTTTGCCATTGATATTAATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGA 77	723 ATAAGGACTITGCCATTGATATTATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGA 78
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                                      Rumsreid, J., Ziegelbauer, K. and Spaltmann, F. Cloning, expression, affinity purification and characterization of polyhistidine-tagged cytosolic Saccharomyces cerevisiae and human inorganic pyrophosphatases for differential screening of compounds for antifungal activity
                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Direct Submission
Submitted (20-NOV-1998) Resea
Box 10179, Wuppertal 42096, O
Location/Qualifiers
                      Rumsfeld, J., Ziegelbauer, K.
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nilarity 100.0%;
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/db_xref="taxon:9606"
/cell_line="BjAB"
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           Score 784;
Pred. No.
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     Mismatches
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GGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTG TCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAA CTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGGCCCCT , product="cytosolic inorganic pyrophosphatase"
(protein\_id="AAD24964.1"
(protein\_id="AAD24964.1"
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(pr 82 302 142 242 182 362 202 482 422 262 382 322 502 602 442 542 782 722 562 662 622 742 682

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PROGRESS
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Sequence
AX192855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                                     TAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACTCA 1105
   TAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGATGTGCAAGGGGAGCAC
                                                                          GAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTTTTAGCACATGCT
                                                                                                             TAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACTCA
                                                                                                                                                                                          ATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGTAGCTTTTCAAAGCTT 1045
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Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15020403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L0875; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 160563 bases at least Q40
Consensus quality: 161175 bases at least Q30
Consensus quality: 161440 bases at least Q20
Insert size: 165756; sum-of-contigs
Insert size: 158385; 9.5% error; agarose-fp
Quality coverage: 6.40x in Q20 bases; sum-of-contigs Quality
coverage: 6.85x in Q20 bases; agarose-fp
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AL355138.18 GI:1
HTG; HTGS_PHASE2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code:
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mmalia; Eutheria; Primates; Catarrhini;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 215049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Street, Waltham, MA 02453, USA
on May 26, 2001 this sequence version replaced gi:8954013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Data
                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                              runs of N, but t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                  Assembly Project.

Consensus quality: 194485 bases at least consensus quality: 199162 bases at least consensus quality: 201282 bases at least consensus quality: 20182 bases at least Insert size: 211948; sum of contigs
                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: hg285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code:
                                                                                                                                                                                                                                                                                                                  Quality coverage: 6.8x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                              Chemistry:
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                                                                                                                                                                                                                      be updated with the finished sequence available and the accession number will
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/db_xref="taxon:9606"
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                                                                                                                                                                                                               GTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCTGGAATACAAGCTGAT 985
GAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAACTTTTAGCACATGCT 114020
                                                             TAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACTCA
                                                                                             TAAATTTGTAGAACTCATCTAACTAAAGTAAATTCTGCTGTGACTAATCCAATATACTCA 1105
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AX014834
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167012)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATENT: WO 9953040-A 23 21-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 357)
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Homo sapiens chromosome
9 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAET; HTGS_ACTIVEFIN
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/db_xref="taxon:9606"
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                              CTGGCTGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTG
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Center Code: JGI
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Quality coverage:
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39820 c 39446 g 43467 t
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/db_xref="taxon:9606"
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SEQUENCE, 41 unordered pieces
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Direct Submission
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/db_xref="taxon:9606"
/chromosome="5"
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                                          /note="assembly_name:Contig25"
11821. .13498
'note="assembly_name:Contig27"
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|3599. .15122
                                                                                                         note="assembly_name:Contig18"
                                                                                                                                                                                                                                        clone="RP11-536N17"
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                                                                                                                                 assembly_name:Contig16"
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187825. .208210
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17433. .19823
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75112. .187724
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3548. .15609
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1424. .117734
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36. .77910
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Homo sapiens chromosome CHROM 10 clone RP11-379018, *** SEQUENCING
IN PROGRESS ***, 117 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-APR-2000) Street, Waltham, MA 024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 205656)
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                                                                                                                           consists of 117 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                             NOTE: This is a 'working draft' sequence consists of 117 contigs. The true order o
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                    6431:
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                                                                                                                                                                                                                                                                                                        Center project name:
                                                                                                                                                                                                                                                                                                                            Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                          Web site:
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                                                                                                                                                                                                                                                                                                                  Project Information
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On May 16, 2001 this sequence version replaced gi:8389438
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                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of Il contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                          as soon as it is available and the be preserved.
                                                                                                                                                                                                                                                                           This record will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 195126)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 195126)
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     15992
                                                                                                                                            1102: contig of 1102 bp in length 1202: gap of unknown length 2394: contig of 1192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 990315 Consensus quality: 188219 bases at least Consensus quality: 189037 bases at least Consensus quality: 190569 bases at least Insert size: 194225; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 990315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: GTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 6.7x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: gtc-segcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTGS_DRAFT; HTGS_FULLTOP
                                              4: gap of unknown l
4: contig of 1250 k
4: gap of unknown l
0: contig of 1186 k
                                                                                                                                                                                                                                                                              be updated with the finished sequence
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Primates;
                         gap
  contig
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10 clone RP11-408L20, WORKING DRAFT
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unknown leng
of 10862 bp
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n length
6 bp in length
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COMMENT

TITLE

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TITLE
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                                                                                                                                                                                                                                                                                                                                                      384 AGACTTGGGAAGACCCAGGGCACAATGATAAAACATACTGGCTGTTGTGGTGACAATGACC 443
                                                                                                                                                                                                                                                                                       444 CAATTGATGTGTGTGAAATTGGAAGCAAGGTA 475
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                      HTG 26-MAY-2001 HOMO sapiens chromosome 10 clone RP11-367H5, WORKING DRAFT SEQUENCE, 33 unordered pieces.
                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 215049)
 Genome
                  Smith, D.R.
                                                                              Homo sapiens
                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT;
                                                                                                                               AC067749.4 GI:14209706
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Therapeutics Corporation Sequencing Center: Human Genome
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46055 c 45277 g 49797 t
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clone_end:SP6"
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clone_end:T7"
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/db_xref="taxon:9606"
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118106. .195126
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70021. .92732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig32"
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118105: gap of unknown length
195126: contig of 77021 bp in
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92732: contig of 22712 bp in length
92832: gap of unknown length
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contig of 15642 bp in length
gap of unknown length
contig of 22695 bp in length
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Pred. No.
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                                                Catarrhini; Hominidae;
                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                               HTGS_FULLTOP
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8.5e-36;
ches 0;
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JOURNAL
REFERENCE
AUTHORS
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On May 26, 2001 this sequence version replaced gi:8954013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished 2 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence this record will savailable and the accession number will
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Chemistry: Dye-terminator Big Dye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: GTC
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                       /note="assembly_name:Contigl34
clone_end:SP6"
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/db_xref="taxon:9606"
/chromosome="10"
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/clone_lib="RPCI-11"
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note="assembly_name:Contig135"
                                                            note="assembly_name:Contig127"
                                                                                    'note-"assembly_name:Contig124"
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:e="assembly_name:Contig12"
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                                                                                                                                                                                                                                                                                                                 e="assembly_name:Contig63"
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Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas A visis T
                                                                                      2 (bases 1 to 155645)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Brown, A., Castle, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Cooke, P., DeArellan, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Cooke, P., Dearellan, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Cooke, P., Dearellan, K., Dewar, K., Dowle, B., Case, D., Case
                                                                                                                                                                                                                                         Homo sapiens, clone RP11-8D23
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (1 (bases 1 to 155645)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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/note="assembly_name:Contig136"
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                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stange-Thomann, N., Stojanovic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Testaye, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson, K., Pollara, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrow, J., Naylor, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McEwan, P., McGurk, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 155045; sum-of-contigs
Quality coverage: 12.1 in Q20 bases; agarose-fp
Quality coverage: 11.9 in Q20 b
Quality coverage: 12.1 in Q20 bases; agarose-fp
Quality coverage: 12.1 in 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L2966
Center clone name: 8_D_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 153969 bases at least Q40 Consensus quality: 154547 bases at least Q30 Consensus quality: 154815 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead'Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 152000;
Insert size: 155045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 242: gap of
243 889: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                     2504
                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
990. 1642;
           /note="assembly_fragment"
4143. .155645
                                                                                                                                                                                                                          /note="assembly_fragment"
1743. .2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="RP11-8D23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 4142: gap of 10
3 155645: contig of
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male.BAC"
                                                                                                           'note="assembly_fragment'
                                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1742: contig of 653 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3280:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2503:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J: contig c
J: gap of
3180: cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 100 bp
contig of 762 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 100 bp
contig of 647 bp in length
of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 142 bp in length
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Norman,C.H., O'Connor,T., O'Donnell,P.,
Norman,C.H., O'Connor,S., Severy,P.,
V., Riley,R., Roy,A., Santos,R., Severy,P.,
Ojanovic,N., Subramanian,A., Talamas,J.,
Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anovic, N., Subramanian, A., Talama: Vassiliev, H., Vo, A., Wheeler, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
of 661 bp in
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BASE COUNT.
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KEYWORDS
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AC025103
                                                                                                                                                                                                      COMMENT
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAI
                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76646 CCTGTGAATCTGCCTGCAC 76664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834 AGAGCCCCTTCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCAC 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894 CCTGTGAATCTGCCTGCAC 912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACO25103 70575 bp DNA HTG 13-JUL-2000 HOMO SAPIENS CLONE RP11-25A15, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G.,
Camponiano A Carta T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d (bases 1 to 70575)
Birren, B., Linton, L.,
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HTG; HTGS_PHASE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campopiano, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-25A15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                            Submitted (05-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S
                                                                                                                                                                                                                                                                                                                                               Roy,A., Santos,R., Schauer,S., Se
Stange-Thomann,N., Stojanovic,N.,
Tesfaye,S., Theodore,J., Tirrell,
                                                                                                                                                                                                                                                                                                                                                                                                                Pisani,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarthy, M.,
                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                    Young,G.,
                                                                                                                                                                                                                                                                                                                          Vassiliev, H., Viel, R.,
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Center project name: L4527
                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                             Center code: WIBR
                                                                                                                   Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J., Gardyna,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
32211 c 29880 g 43751 t
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                                                                                                                                                                                                                                                                                                    Zainoun, J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lieu,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iliev, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castle, A.,
                            Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grant, G., Hagos, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu, G., Locke, K., Macdonald, P., Marquis, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                          Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson, R., Jones, C.,
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                                                                                                                                                                                                                                                                                                                                                    Tirrell, A., Travers, M.,
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Severy, P., Spencer, B.,
N., Subramanian, A., Talamas, J.
N., Trigilio, J.
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NOTE: This record contains 75 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33900 TGTTGTGGTGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGA 33959
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Bovine inorganic pyrophosphatase mRNA sequence.
M95283
                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                       BC010468 1243 bp mRNA
Mus musculus, RIKEN CDNA 2010317E03
Mus musculus, RIKEN CDNA 2010317E03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93077559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular cloning and functional expression mammalian inorganic pyrophosphatase J. Biol. Chem. 267, 24641-24647 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1266)
Yang, Z. and Wensel, T.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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Bos taurus retina cDNA to mRNA.
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              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                          Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                BC010468.1
                                                                                                                                                                                                                                              BC010468
                                                                                                                       Strausberg, R.
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                        Direct Submission
                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                          Institute, 31 Center Drive, Room 11A03,
                                                                                                                                      (bases 1 to 1243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396
cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="retina"
239 c 300 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2. ; Mismatches
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                                                             Bethesda,
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Matches Query Match Best Local

Similarity

3.9%;

Score 50;

DB 10; 3e-14;

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Conservative

·0;

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606 TGGTTTAGAAGGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGC 653 TGGTTTAGAAGGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGC

655 702

RESULT 25 ACO25103/c

REFERENCE

(bases 1 to 70575)

TITLE

Birren,B., Linton,L., Nusbaum,C. Homo sapiens, clone RP11-25A15 Unpublished

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

and

Lander, E

AUTHORS JOURNAL

REFERENCE

(bases 1 to 70575)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

SOURCE VERSION DEFINITION

ORGANISM

Homo sapiens

KEYWORDS ACCESSION Locus

HTG; AC025103.1 AC025103 Homo AC025103

HTGS\_PHASE0.

GI:7158913

sapiens

70575 bp clone

ор DNA RP11-25A15,

LOW-PASS SEQUENCE SAMPLING

13-JUL-2000

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FEATURES
                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I:M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 10 Row: f Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/contact: villalon@bcm.tmc.edu.
villalon, D.K., 'Luna, R.A., Hale, S.M., Hul
A.M., 'Holloway, M., Telford, B, Hodgson, A.
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center
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                                                                                                        366
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:6716 IMAGE:3585780"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old.virgin mouse. Taken by biopsy."
/clone_ilb-"NCI_CGAP_Maml"
/lab_host="DH10B"
                                                                                                                                                                                                          /translation="msgfsseeraapftleyrvflknekggyispfhdvpiyadkdvf
Hmvvevprwsnakmeiatkdplnpikgdvkkgklryvanlfpykgyiwnygaipqtwe
Dpghsdkhtgccgdndpidvceigskvcargeiirvkvlgilamidegetdwkviain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="LocusID:67895"
/db_xref="taxon:10090"
                                                                                                  PTDVDKWFHQQKN"
270 c 3
                                                                                                                                                        IIKSTHDYWKALVTKKTDGKGISCMNTTVSESPFKCDPDAAKAIVDALPPPCESACSL
                                                                                                                                                                                    VDDPDAANYKDISDVERLKPGYLEATVDWFRRYKVPDGKPENEFAFNAEFKNKDFAVD
                                                                                                                                                                                                                                                                                                                   /product="RIKEN cDNA 2010317E03 gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           /codon_start=]
                                                                                                                                                                                                                                                                                            /db_xref="GI:14714657"
                                                                                                                                                                                                                                                                                                                                                                                                                           note="Vector:
                                                                                                     310 g
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Length 1243;
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy, T., Naylor, J., Norman, C.H
O'Neil, D., Olivar, T.M., Oliver, J
Pisani, C., Pollara, V., Raymond, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCartny,..., Meneus,L., Minovu,...,
Meldrim,J., Meneus,L., Minovu,...,
Mavlor,J., Norman,C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tesfaye, S., Theodore, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nttp://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This record contains 75 individual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Santos, R., Schauer, S.,
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3738:
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contig of 842 bp
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                                                                   CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:12831924.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
regions
               This sequence was finished as follows unless otherwise noted: all
                           corresponding to the overlapping clone, only a small overlap as described above.
                                           variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                               Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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62985: contig of 858 bp
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63913: contig of 828 bp
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58286: contig of 826 bp in length
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59224: contig of 838 bp in length
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55470: contig of 848
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64873: contig of 860
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30); an attempt was made to resolve all sequencing problems,
as compressions and repeats; all regions were covered by at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP13-63115 is from the library RPCI-13.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was generated from part of bacterial clone contichromosome X, constructed by the Sanger Centre C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISSPROT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the entire insert of clone RP13-63I15
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                                                                                                                                                                                                                                                  6009
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/db_xref="taxon:9606"
                                                           /note="L1PA15 repeat: matches 1412. .3280 of consensus"
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                       "THE1B repeat: matches 1.
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/note="LlM4 repeat: matches 4363. .4484 of consensus"
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                                                                      'note="L2 repeat: matches 2604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LlP_repeat: matches 1450. .1858 of consensus"
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3346"
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5. .43740
e="MER11C repeat: matches 3. .1071 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="L1PA3 repeat: matches 4051.
8. .29237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="L1MA4A repeat: matches 6194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="LIPA3 repeat: matches 5826.
9. .33467
e="LIPA5 repeat: matches 1843.
                                                                                                                                                                                                                                         e="MIR repeat: matches 33.
7. .51235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="L1PB3 repeat: matches 4770.
1. .42634
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- "L1ME2 repeat: matches 4395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p="MIR repeat: matches 42. .252 of consensus"
3. .39349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ="L1PA16 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "MIR repeat: matches 13. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                    -"L1PA16 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "L1PA16 repeat: matches
                                                                                                                                                                                                                                                                                  -"AluY repeat: . .50115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "L2 repeat: matches 2595. .2668 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                     .41PA7 repeat: matches 5152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .42595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .39056
                                                   .54049
                                                                                                                                               .53083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .24916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27153
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                                                                                                                       repeat: matches 2295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 1778.
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                                                                                                                                                                                                              repeat: matches 5837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 5892. .6146 of consensus
                                                                                                                                                                  repeat: matches 6149.
                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 5552.
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                          100% conserved"
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                                                                                                                  .2380 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4448 of
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                                           MEDLINE
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DEFINITION
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Matches '25; Conserv
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Rosenthal, A.,
Direct Submiss
  20287777
2 (bases 1 to 61946)
Blechschmidt, K., Nordsiek, G., Drescher, B., Weber, J.,
Blechschmidt, K., Nordsiek, G., Drescher, B., Weber, J.,
VASDO, M.-L., OSOEgawa, K. and Soeda, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 61946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 21q22.2, complete sequen
                                                                                                                                                                Reinhardt,R. and Yaspo,M.Laure.
The DNA sequence of human chromosome
                                                                                                                                                                                                                                                                                                 Shintani, A., Sasaki, T., Nagamine Antonarakis, S.E., Minoshima, S.,
                                                                                                                                                                                                                                                                                                                                            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M.B., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Kawasaki,K., Asakawa,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Park, H.-S., Toyoda, A., Is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF020802
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                                                                                                               and sequencing consortium Nature 405 (6784), 311-319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1MC4 repeat: matches 6608. .6696 of consensus"
7307. .67648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1M4c repeat:
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54804. .54897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L1MA8 repeat: matches 5534. .6285 of consensus"
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7324. .57446
                                                                                                                                                                                                                                 Riesselmann,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:13957611
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                                                                                                                                                                                                                                                          Kauer, G., Bloecker, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0%;
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                                                                                                                                                                                                                                                                                                                           Sasaki, T., Nagamine, K., Mitsuyama, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="MLT1J
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                                                                                                                                                                                                                                                                             Brandt, P.,
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Pred. No.
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                                                                                                                                                                                                            Nizetic, D.,
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21 clone cosmids Q98A3 and c103C0352 map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor, T.D.,
                                                                                                                                                                                                                               Scharfe,M., Schoen,O., Desario,A., oecker,H., Ramser,J., Beck,A., Klages,S., Dagand,E., Haaf,T., Wehrmeyer,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                           Taudien, S., Blechschmidt, K.,
                                                                                                                                                                                                                                                                                                   Shimizu, N
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0.15;
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                                                                                                                                                                The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .261 of consensus"
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Indels

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consensus"

Nordsiek,G

Soeda, E.,

chromosome

21 mapping

Schattevoy, R.,

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RESULT 28
HS1042K10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 GAAAACCAGAAAATGAGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blechschmidt,K., Nordsiek,G., Drescher,B., Weber,J., Schattevoy,R., Rosenthal,A., Yaspo,M.-L., Osoegawa,K. and Soeda,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biotechnology, Beutenl
3 (bases 1 to 61946)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence from 22q13.1-13.2 Contains th
                                                                                                                                             During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                           This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL022238.1 GI:4176442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone RP5-1042K10 on chromosome 22q13.1-13.2 Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS1042K10 184180 bp
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                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB10 1SA,
     http://www.sanger.ac.uk/Projects/C_u
from the library RPCI-5 constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jan 22, 1999 this sequence version replaced gi:3927920.
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the library
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UK. E-mail enquiries: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .61946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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  RPCI-5
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     elegans/wormpep
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          Park Cancer
                                RP5-1042K10 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RP5-1042K10 It may be shorter because we only sequence over sections once, or longer because we arrange for a small over
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: pCYPAC2
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                                                                                                                                                                                                                                                                                                                                                                                                     /note="supported by GENSCAN and FGENES match: ESTs: Em:AA615306 Em:AA065323 Em:W80019 Em:N75651 Em:AA747718 Em:AA354286"
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complement(5, .477)
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/db_xref="taxon:9606"
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                                                                                  STKQEAAKAQTALH"
                                                                                                                             GHNPTHLSNKMWKNHISSRNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRGWGTQDSRL
                                                                                                                                                   TDHQLLRDNTTGSNSSLNTSLPSPGAWPYSASDNSFTNVHSTSAKFPDYKSTWSPDPI
                                                                                                                                                                           AKSPPTNKIGSKSSNASWPPEFQPGVPWKGIQNIDPESDPYVTPGSVLGGTATSPIVD
                                                                                                                                                                                                    SMMEGLPSVATQEANMHKNGAIVAPGKTRGGSPYNQFDIIPGDTLGGHTGPAGDSWLP
                                                                                                                                                                                                                       PKPHLDNMVPNALNVGLPDLQTKGPIPGYGSGFSSGGMDYGMVGGKEAGTESRFKQWT
                                                                                                                                                                                                                                                                                           /product="dJ1042K10.4 (novel protein)"
/protein_id="CAA18263.1"
/db_xref="GI:4176443"
                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: STS: Em:B14103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 61.
                                                                                                          ASASTWSDGGSVRPSYWLVLHNLTPQIDGSTLRTICMQHGPLLTFHLNLTQGTALIRY
                                                                                                                                                                                                                                          /translation="RKISQAVRQQQEQQLARMVSALQQQQQQQQQQRQPGMKHSPSHPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="dJ1042K10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oin(<3190. .3233,3378.
4733. .14879,15130. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="dJ1042K10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oin(3190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="FLAM_C repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Alux repeat: matches 1.
                                         /note="MIR repeat: matches
                                                                                                                                                                                                                                                                     db_xref="SPTREMBL:095512"
                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .184180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te="MIR repeat: matches 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : GSS: Em:B14103"
3190. 3233,3378. 3561,10740.
.14879,15130. 15225,17511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 140. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78. .3561,10740. .10877,13045. .1322
.15225,17511. .17735,18170. .18240,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches
                                           31. .226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .309 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .297 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .215 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .71 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .10877,13045. .13221.
.17735,18170. .18240,
.5894 of consensus"
                                           of consensus"
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misc\_feature

note="match: GSS: Em:AQ627708" 3904. .4459

. 4574

Indels

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Gaps

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Length 184180;

HTG DRAFT

03-FEB-2001 SEQUENCE, 27

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alux repeat: matches 1. .294 of consensus"
complement(20915. .21365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ549653"
3974. .3998
                    /note="MER5A repeat: matches 119.
complement(25351. .25770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3974. 3998
/note="MER46A repeat: matches 149. .167 of consensus"
                                                                                                                                                                 complement(2311]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :omplement(12001
                                                                                                           note="AluYb8 repeat: matches 1.
                                                                                                                                                                                                                                                      note="AluY repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 51. .262 of consensus"
                                                                                                                                            note="match: GSS: Em:AQ356569"
                                                                                                                                                                                                                                                                                           note="MER44A repeat: matches 192.
                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: GSS: Em:AQ170974"
                                                                                                                                                                                                                                                                                                                              ote="Alu repeat: matches 244. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ote="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plement(14139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9. .8547
te="AluYa8 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te="AluJo repeat: matches 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            te="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               te="L2 repeat: matches 2062:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5. .7010
te="Charlie2 repeat: matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...5553
Le="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5. .5106
ce="Charlie2 repeat: matches 34. .149 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te="AluSg repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="AluSx repeat: matches 3.
                                                                                                                                                                                                                     e="MER44A repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .18860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IR repeat: matches 33. .134 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   narlie2 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              igger4(Zombi) repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          copies 2 mer tt 64 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 2609. .2710 of consensus
                                                                      repeat: matches 6053.
                                                                                                                                                                                repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS:
     STS: Em: AA699725"
                                                                                                                                                                                                                                                                                                                                                                                               GSS: Em: AQ002626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Em: AQ523109"
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                                                                                                                                                                                                                                                        .310 of consensus"
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                                                                                                                                                                                 .299
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                                                                                                                                                                                                                                                                                                                                                                  .293 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .294 of consensus*
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                                                                        ,6324 of
                                                                                                                                                                                                                                                                                           .243 of consensus"
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AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 136023 TTTCATATCTCAACTAAGATAA 136044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1129 TTTCATATCTCAACTAAGATAA 1150
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                                                                                                                                                                                                                                                                       Center project name: RP23-114F14
Center clone name: RP23-114F14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                 On Feb 3, 2001 this sequence version replaced gi:11276150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-NOV-2000) Lita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Zutavern, T
                                                                                                                                                                                                                                                                                                                                                                                                 Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center, Cold Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC084825.2 GI:12658007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC084825
                                                                                                                                                                                                                                                                                                                            Web site: http://www.cshl.org/genseq
Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Genomic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez,S:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dedhia,N.N., de la Bastide,M., Huang,E.N., King,L., Kirchoff,K.A., Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1cCombie, W.R
                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                       as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 216425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 216425)
   42730
43017
56376
                                                       24309
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                                                                                                                                                                                                                                                                                                                                                                  code: CSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="22
26107. .26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="35 copies 2 mer gt 68 conserved"
complement(27815, .28237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match:
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Shah, R.S., Spiegel, L.A.,
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Balija, V

Toth, K., Vil, M.D.

Hazen Genome Sequencing 1 Bungtown Road, Cold Spring

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are unknown.

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VERSION
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AC073945 232710 bp DNA
Mus musculus clone RP23-171e18, W
unordered pieces.
AC073945.18 GI:14861741
AC073945.18 GI:14861741
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                        Conservative
                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-114F14"
49581 c 47418 g 5405
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 232710)
Song,L., Jiang,X. and Roe,B.A.
Mus musculus BAC Clone rp23-171e18
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-171e18"
/44003 c 43046 g 7095
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Jordon 1920 John Termer 1 phase: 0"  Jevidence-not_experimental  4584. 4601	3702. 3821  /note="GRAIL, score = 60.000%, comment = good" /evidence=not_experimental	region complement(2981, .3198)  /rpt_family="MIR"  /evidence=mot_experimental  /rpt_family="MIR"	fa.enfa.	/evid 2422. /rpt_ /evid 2570	_region complement(13491559) /rpt_family="MLT1B" /evidence=not_experimental /region complement(20552418) /rpt_family="MLT1A1"	<pre>/rpt_ramily="ML71B" /evidence=not_experimental .region complement(10461348) /rpt_family="AluJo" /evidence=not_experimental</pre>	region 160. 289 /rpt_family="FLAM_A" /retidence=not_experimental /evidence=not_experimental region complement(917. 967)	2. 46430 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Cosmid Q98A3 (AF020802)"		Location/Qualifiers 1. 323000	07745 Jena, GERMANY 07745 Jena, GERMANY Complete contig available via ftp: ftp.ebi.ac.uk/pub/databases/embi/genomes/hsapiens/contigs/aj229040/	al,A., Yaspo,M.L., Osoegawa,K. and Sc ) Karin Blechschmidt, Institute of Mc f Genome Analysis Boutenborgstrasso	n AML1 and C	mates; Catarrhini; Hominidae;	ns Metazoa: Chordata:	HS229041 323000 bp DNA PRI 22-MAY-1998 HOMO sapiens 959 kb contig between AML1 and CBR1 on chromosome 21922; segment 1/3. AJ229041 AJ229040 AJ229041.1 GI:3153101
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/ IPC_ramily = Alusy /evidence=not_experimental complement(1864618944) /rpt_family="Alusc" /evidence=not_experimental	/rpt_family="Aludb", /rpt_family="Aludb", /evidence=not_experimental complement(1765717936)	/ev.vence-no.cexper.imentar complement(1616016454) /rpt_family="AluSp" /evidence-not.experimental /evidence-not.experimental	/ipt_remail_ 12 /evidence=not_experimental 1568715846 /note="GRAIL, score = 65.000%, comment = good"	<pre>/note="GenScan, score = 3.65%, comment = Terminal_exon 228 bp frame: 2 phase: 0" /evidence=not_experimental complement(1563415678)</pre>	xperimental 8. 14380) usx" xperimental	<pre>complement(122251238) /rpt_family="L2" /evidence=not_experimental 1229412390 /note="GRAIL, score = 60.000%, comment = good"</pre>	/evidence=not_experimental complement(11856. 12044) /rpt_family="12" /evidence=not_experimental	/rpt_family="ML71B" /evidence=not_experimental complement(11094 . 11392) /rpt_family="AluSq"	<pre>complement(967910211) /rpt_family="L1MD3" /evidence=not_experimental complement(1072111087)</pre>	<pre>complement(90659199) /rpt_family="MER58B" /evidence=not_experimental</pre>	/evidence=not_experimental complement(85178768) /rpt_family="MLTZG" /rpt_dence=not_experimental	vidence= 19689 ote="Gen	lement(599 _family="M _family="M _lence=not_ _ 6647 6647	perimental  .5823) ore = 84.000%, comment = e: perimental	<pre>/note="GRAIL, score = 43.000%, comment = marginal" /evidence=not_experimental 50235134 /note="xpound exon prediction, score = 85% (0%)"</pre>	<pre>/note="GRAIL, score = 48.000%, comment = marginal" /evidence=not_experimental 4671   4730 /note="GRAIL, score = 84.000%, comment = excellent" /evidence=not_experimental 4999   5277</pre>

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RESULT 32
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                                   Homo sapiens genomic DNA, chromosome 21q, section 68/105. AP001724 AL163269 BA000005 AP001724.1 GI:7768721
  Homo sapiens DNA.
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/evidence=not_experimental
complement(23334. .23382)
/rpt_family="L2"
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complement(23681. .23784)
/rpt_family="L2"
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frame: 0 phase: 2"
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/db_xref="taxon:9606"
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complement(25717. .25835)
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/evidence=not_experimental
complement(22957. .23069)
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denscan, score = 7.63%, comment = Initial_exon 116
                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                            /note="GenScan, score = 2.49%, comment =
pp frame: 1 phase: 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="G to A in Q98A3"
replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="GRAIL, score = 75.000%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="GRAIL, score = 42.000%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
complement(26017: .26086)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="G to A in Q98A3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 .27258
                                                                                                                                                                                                                                                                                                                      Score 22;
                                                                                                                                                                                                                                                                                                                                                                                                       phase:
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                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                       Length 323000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comment = excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comment = marginal shadow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial_exon 116
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 340000)
Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, Ohki, M., Takagi, T., Sakaki, Y., Taudlen, S., Blechschmidt, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park, H.S., Toyoda, A., Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Submitted (10-APR-2000) and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S:, Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on May 30, 2000 this sequence version replaced gi:7717338. The chromosome 21 mapping and sequencing consortium consisting of *RIKEN Genomic Sciences Center, Human Genome Research Group, *Sagamihara 228-8555, Japan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antonarakis, S.B., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson,D., Reichwald,K., Rump,A., Schillhabel,M.,
Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patterson,D., Reichwald,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * Institute of Molecular Biotechnology, Genome Beutenbergstrasse 11, D-07745 Jena, Germany, 
* e_mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yaspo,M.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asakawa, S., Shintani, A., Sasaki, T., Nagamine,
                                                                                                                                                                                                                                                                                                                                                                                              Mascheroder Weg :
Info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60-8582, Japan,
e.mail: nshimizu@dmb-med.keio.ac.jp
URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e mail: hattori@gsc.riken.go.jp
URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                    Ihnestrasse 73, D-14195 Berlin, Gerr e.mail: info-chr21emolgen.mpg.de uRL: http://chr21.rz-berlin.mpg.de/L163269: Submitted (10-Apr-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keio University School of Medicine,
                                                                                                                                                                                                                                                                                                               Max-Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany,
                                                                                                                                                                                                                                                                                                                                                                             URL:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Dept. of Genome Analysis,
heroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
                                                                                                                                                                                                                                                                                                                                                                        http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://genome.imb-jena.de/
                                                       /note="Accession No. AF015720"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Menzel, U., Delabar, J., Kumpf, K., Lehmann, R.
                                                                                                                                                                                                              .340000
                                                                                                                               .53351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Totoki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schillhabel, M. and Schudy, A. 21. The chromosome 21 mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Biology, * Tokyo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K., Mitsuyama, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schudy, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soeda, E.
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repeat\_region

'note="AluJo"

repeat\_region

'note="AluSx"

epeat\_region

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complement(14684. .14770)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2741. .3129)
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                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                               RESULT 3
CNSO6IA0
LOCUS
                                                                                                                                                                                                                                                                                Db 125791 GAAAACCAGAAAATGAGTTTGC 125770
                                  REFERENCE
                                                                                                                                   VERSION
                                                                                                                                                 ACCESSION
                                                                                                                                                                                  DEFINITION
                  AUTHORS
                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                Saccharomyces bayanus
Eukaryota; Fungl: Ascomycota; Saccharomycotlna; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 958)
Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P.
                                                                                                                                                                                                 CNS06IA0
                                                                                                   Saccharomyces bayanus.
                                                                                                                                   AL400030.1 GI:12155369
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                           S06IA0 958 bp DNA STS 10-JAN-2001 end of clone AS0AA019A04 of library AS0AA from strain CLIB Saccharomyces bayanus, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_type~DISPERSED complement(14845. .15169)
                                                                                                                                                                                                                                                                                                                                                                                                                                20647. .20954
/note="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(19309. .19427)
                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="SINE/Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Accession No. AF020803"
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db_xref="taxon:9606"
chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1ME3A"
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note="(TAAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE.
Segrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic Exploration of the Hemiascomycetous Yeasts: 1. yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic Exploration of the Hemiascomycetous Yeasts: Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wincker, P. and Weissenbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malpertuy, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de-Montigny, J., Dujon, B., Durrens, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Souciet, J.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida tropicalis and Yarrowia lipolytica: Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angusta, Debaryomyo
Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                       binding protein dependent transport protein; catalase; catb; peoR-family transcriptional regulator; gas vesicle synthesis protein; glycerol-3-phosphate debydrogenase; gvpA; gvpF; gvpG; gvpJ; gvpK; gvpD; gvpS; membrane protein; methyltransferase; gvpJ; gvpK; gvpD; membrane protein; methyltransferase; gereted cellulose-binding protein; secreted chitosanase; socute-binding endo-1, 4-beta-xylanase; short chain oxidoreductase; solute-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
transcriptional regulator; transmembrane
                                                                                                                                                                                                      AL132973.1 GI:6434710
2-hydroxyacid-family dehydrogenase;
                                                                                                                                                                                                                                                                                        Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actis var. lactis, Kluyveromyces marxianus var. marxianus
                            ipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 958)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to Saccharomyces cerevisiae ORF YBR011c
IPP1 ; inorganic pyrophosphatase, cytoplasmic ]
1 putative frameshift(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharomyces bayanus"
/strain="CLIB 533"
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/clone="AS0AA019A04"
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                                                                                                                                                                                                                                                                                                                       39525 bp
                         tellurite resistance protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aigle, M., Artiguenave, F.,
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Pred. No.
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..21;
                                                                                                                                                                                                                    anti-sigma factor antagonist;
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Lepingle,A., Llor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hansenii, Pichia sorbitophila,
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     efflux protein;
                                 terD; tetR-family
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                                                                                                                                                                                                                                                                                                                             23-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-NOV-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBH0 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, colney, Norwich; Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the BBSRC
Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor sequencing at The Sanger Centre is funded by the {\tt BBSRC} and Beowulf Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliver, K. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The length in codons is given for each CDS.
Usually the highest scoring match found by fasta o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colney, Norwich; Norfolk NR4 7UH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       small overlap between neighbouring submissions Cosmid F91 Overlaps with cosmid StF15 on the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upstream initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jun/cgi-bin/frameplot.pl.
correct initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        program of Bibb et al., Gene 30:157-66(1984) as implemented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cosmid F91 Overlaps with cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 39525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   more significant matches with motifs in the PROSITE database also included but some of these may be fortuitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases
                         /note-"SCF91.01, terD, tellurite resistance protein, /note-"SCF91.01, terD, tellurite resistance protein, partial CDS, len: > 81 aa. Highly similar to many tellurite resistance proteins including: Serratia marcescens SW:TERD_SERMA(EMBL:L38824) tellurium resistance protein TerD (192 aa), fasta scores opt: 398 z-score:
                                                                                                                                                                                                                            /gene="terD" complement(1.
                                                                                                                                                                                                                                                                                                                                /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
                protein TerD (192 aa),
                                                                                                                                                                                                   /note="nominal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 rocation,
                                                                                                                                                /gene="terD"
                                                                                                                                                                                                                                                                                                            clone="cosmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
                                                                                                                                                                                                      overlap with cosmid StF56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: We may not have predicted the
                      fasta scores opt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AseI-F genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
```

CDS

```
putative secreted cellulose-binding protein SCI11.23 (356 aa), fasta scores opt: 349 z-score: 417.9 E(): 6.7e-16 32.2% identity in 227 aa overlap: Also weakly similar to chitin-binding proteins e.g. Streptomyces olivaceoviridis TR:054501(EMBL:X78535) chitin binding protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance (192 aa), fasta scores opt: 393 z-score: 534.8 E(): 2e-22 71.3% identity in 80 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541.4 E(): 8.8e-23 72.5% identity in 80 aa overlap and Escherichia col TR:CAB42998(EMBL:AJ238043) tellurite
                                                                                                                                                                                                     Contains possible membrane spanning hydrophobic do possible N-terminal signal sequence and a PS00216 transport proteins signature 1. Also contains a prociled-coil from 76 to 107 (32 residues)."
                                                                                                                                                                                                                                                                                                                /note="SCF91.04c, possible membrane protein, len:
Contains possible membrane spanning hydrophobic do
                                                                                                                                                                                                                                                                                                                                                                                    complement(3000. .5156)
/gene="SCF91.04c."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2121. .2807)
/gene="SCF91.03c"
                                   /product="putative membrane protein."
/protein_id="CAB61161.1"
/db_xref="GI:6434714"
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCF91.04c."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVVDPASRNYGCWERWGDDFQNPAMADEDPMCWQAWQDDPNAMWNWNGLYRNGSAGDF
EAVVPDGQLCSGGRTESGRYNSLDAVGPWQTTDVTDDFTVKLHDQASHGADYFLVYVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein, len: 228 aa. Similar to several including:
Streptomyces coelicolor TR:CAB50949(EMBL:AL096849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SCF91.03c"
complement(")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(312..2057)
/gene="SCF91.02c"
/note="SCF91.02c, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="IHDAENRGQSFGQVRNAFIRVVNQANNQELARYDLSEDASTETA
MVFGELYRHGAEWKFRAVGQGYASGLAGIAADFGVNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2814. .2818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative secreted
/protein_id="CAB61160.1"
/db_xref="GI:6434713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       possible N-terminal signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="SCF91.03c, possible secreted cellulose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JPRPLQHPNNVWALHGLHECLVRLGRAGEVRIVAQQLRFAAALADVPVEASCFCRLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \AFAALERSVELDDNLPYDEPWGWMQPTRHAYGALLLEQGRTAEAEAVYRADLGLDDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRVESPPMADWLEAFLAMRVHVLIRFGRWTDILALPLPDDPRLYCVTTAMLHYARGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>APDDLDVAALYADALMNLTPWQLWDLRTGLPAEGARTLAAKEVLDRALAAEGGRDHP</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDRTHAAVERAHALAGRATPAERALIDALRARYPQASAVEDCSVWNAPYADGMRAVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGLVWTYAFHHEEAVACFEAAVAADPDCAMAHWGIAHALGPNYNKPWDAFDTEELTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein SCF91.02c"
/protein_id="CAB61159.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SCF91.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="tellurite resistance protein (fragment)"
/protein_id="CAB61158.1"
/db_xref="GI:6434711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
translation="MGHNRRRPTGARRATFGAVALILGGSGLVAVNVFASATESGNP"
                                                                                                                                           transl_table=11
                                                                                                                                                                            /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SATGRVAEAETERDLFRAAVDRVPGSRTLFNNTCADILAIASAMLDGELEYRRGNHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MTCHDRAKIQLAGRARRATTLVLSTLAAVLLTLIPWSGTAVAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MRPSAEALRDRPRCGIRPSMDYYDLGRHGRPVTTSSPEAQRWFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Q54501(EMBL:X78535) chitin binding protein precursor 201 aa), fasta scores opt: 203 z-score: 249.8 E(): .5e-06 29.38 identity in 222 aa overlap. Contains a ossible N-terminal signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGFDPATQALTWGELQQVARTGSYGPSQNYEIPVSTSGLTGRHVVYTIWQASHMDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THLMEMSPTPEAALAVADRLRGLVPDAGHLLHMPSHLEVLCGDYRRVVSDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JARSGAMNFYTLYRAHNHHFKIYGAMFLGRYEVALDAAARLEASVPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2057)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellulose-binding protein."
                                                                                                                                                                                                                                        Also contains a probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 aa."
                                                                                                                                                                                                                                                                                                                domain,
```

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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxyacyl-CoA dehydrogenase (329 aa), fasta scores opt: 308 z-score: 335.0 E(): 2.8e-11 31.8% identity in 333 aa overlap. Contains a Prosite hit to PS00059 Zinc-containing alcohol dehydrogenases signature and a Pfam match to entry PF00107 adh_zinc, Zinc-binding dehydrogenases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00216 Sugar transport proteins signature complement(5163. .5167) complement(5266. .6279)
                                    RGVDYDGGWAEYALCAADAMTPLPDAIPFEQGAIIPDAVSTPWGAITETGEVRPAEAV
GVWGVGGLGVHAVQLLRAIGACPVVAVDPSPVARERALAAGADLALDSADPEFRQKVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SCF91.05c, possible Zinc-containing dehydrogenase, len: 337 aa. Similar to many dehydrogenases including: Alcaligenes eutrophus SW:ADH_ALCEU(EMBL:J03362) alcohol dehydrogenase (EC 1.1.1.1) (366 aa), fasta scores opt: 272 z-score: 296.1 E(): 4e-09 27.0% identity in 371 aa overlap and Streptomyces coelicolor TR:Q53927(EMBL:X62373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLAETGSGLGLWPAAVGGVLFAGGCVLLLRSRRTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVYDVAAPSLEDGGRTVPLFAVDSFPEQLHKPVTDHSDFINVFDEDLMREMVECINSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIESVRPNAVRAPRQQKASTGSFATSCGVNAEGLFNSDNLIAAPGVSNGAHHFHDYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVPLGSSGVAATVDCPDPTERLTAVPEQARPTVDTELAQLDEQIAAAYRGLQEAARAA
DDGTLDEGAILDPLKKERAATIERIAAAIDRAGRRPEGLDALAECTLRRTEVASADAG
AATGGAGLAAAFDFAGVPPVREQAVSVLAPKGRLVLAGLTDKPLTVTDGTRFSYLQQR
                                                                                                                           VHLIDGTLTPLLLRGDTVTLGHEVSGTVAGTGAGVTAWSPGQRVVLHAGERRDGVTYT
                                                                                                                                                                                                             /product="putative Zinc-containing dehydrogenase."
/protein_id="CAB61162.1"
/db_xref="G1:6434715"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCF91.05c."
complement/soff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGDEPVPPAEGQDAGASASAEPRAATTPADAPNAPNAPNAPNNVSGTGAAPAPQAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQANNALASDEDLAAGDTSCADQGDKSSYYWPVLRLQNGSDEQDAQSPGGGIEGNAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSPAQQGQEQGQGQGQEREEGQEQGRQDDEGEAPGDGQQQPGNGGQAGNGPVAADYV
                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                    translation="MAQMLAARLHVPSRTLRLEEVPRPQPGPGEVLVKVEAAGVCLSD"/
                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
```

gene

```
В
                                     Matches
                                             Query Match
Best Local
33904 GGCTTCAGCACCGAGGAGCGC 33924
                  95 GGCTTCAGCACCGAGGAGCGC 115
                                     21,
                                              Similarity
                                     Conservative
                                             1.6%;
                                             Score 21; Pred. No.
                                    0;
                                     Mismatches
                                             DB 1;
18;
                                     Indels
                                     0,:
                                    Gaps
```

Length 39525;

0

```
SOURCE
ORGANISM
                                                                                            REFERENCE
                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                          RESULT 35
AF020801/c
                                                                                                                                                                    VERSION
                                                                                                                                                                              ACCESSION
                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                   SOCOS
                                                                                 AUTHORS
      Homo sapiens
                                                                                                                                                       HTG
                                                                                                                                                                                         complete sequence.
                                                                                                                                                                                                     Homo sapiens chromosome
Shintani,A., Sasaki,T., Nagamine,K.
Antonarakis,S.E., Minoshima,S., Shi
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                    AF020801.2
                                                                                                                                                                                                                 AF020801
                                                                                                                                             human
                                                                                                                                                                                                                 44548 bp
                                                                                                                                                                                                 DNA PRI US-MAI-2001
21 clone cosmid c102A0977 map 21q22.2,
```

RBS gene

Beck, A., Klages, S.,

CDS

```
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
AF176815/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Lo
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Borzym, K.,
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AF176815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blechschmidt, K., Nordsiek, G., Drescher, B., Rosenthal, A., Yaspo, M.-L., Osoegawa, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotechnology, Beutenpergsil. 11, John School on May 5, 2001 this sequence version replaced gi:2801435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-MAY-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF176815 51803 bp DNA PRI 23-DEC-199
Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                              Hu,S.N., Dong,W., Zeng,Y.X., Direct Submission
                                                                                                                                                                                                                                                                              Hu,S:N., Dong,W., Zeng,Y.X., Yu,J. and Yang,H.M. Sequencing and Analyzing of BAC DNA on 3p26
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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/clone="cosmid c102A0977"
/g296 c 9462 g 11891 t
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/db_xref="taxon:9606"
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join(<26286. 26884,31142. 32101,32922. 33084,33
341.67. 34295,35086. 35395,35720. 36043,36366. 37150. 37297,37715. 37851,37954. 38072,38442. 39308. >39491)
                                                                             /organism="Homo sapiens"
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                                                              /map="3p26"
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                                                                                                                                                                                                                                 Yu,J.
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                                                                                                                                                                                                                                 and Yang, H.M.
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Soeda, E.
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Lehrach,H.,
                                                .33084,33451
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                   .38596
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ORIGIN BASE COUNT

13024

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.13048

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12751 g

12980

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/product="putative 8-hydroxyguanine DNA glycosylase"
join(26286. .26884,31142. .32101,32922. .33084,33451. .3
34167. .34295,35086. .35395,35720. .36043,36366. .36650,
37150. .37297,37715: .37851,37954. .38072,38442. .38596,
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FFDNKRTWQWLPRTKLVPLGVNQDLDKEKMLEGRKSNIRKSVQIAYHRALQHRSKVQG
                                        VWAKCRGYPSYPALIIDPKMPREGMFHHGVPIPVPPLEVI
                                                                            SRGTFPEDSSEDTSGTENEAYSVGTGRGVGHSMVRKSLGRGAGWLSEDEDSPLDALDL
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Qy · B Matches Query Match Best Local 23929 56 CTGTGGCAGCGGCGGCAG CTGTGGCAGCGGCGGCGGCAG 76 Similarity Conservative 100.0%; 23909 0; Score 21; Pred. No. Mismatches 18; 9 0; Length 51803; Indels 0; Gaps

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RESULT AL355504

KEYWORDS SOURCE ORGANISM REFERENCE DEFINITION VERSION ACCESSION CUS AUTHORS Eukaryota; Mammalia; I Homo sapiens AL355504.17 complete AL355504 . Human DNA AL355504 Bates, K (bases 1 to 60159) sequence. ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo. 60159 bp sequence from GI:12597083 clone DNA PRI 28-JAN RP11-218A18 on chromosome 28-JAN-2001

COMMENT JOURNAL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk on Jan 29, 2001 this sequence version replaced gi:12580993. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the Direct Submission

corresponding to the overlapping clone, as we only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems such as compressions and repeats, but not necessarily within known variation annotation may not be found in the sequence corresponding to the overlapping clone, as we submit sequences submission with

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FEATURES
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""" """ SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-218A18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-270H22 is at 60060 in this sequence. The true right end of clone RP11-380B4 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mapping Group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ip://www.chori.org/bacpac/home.htm
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db_xref="taxon:9606"
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e="MLT1J repeat: matches 273. .354 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="MLT1J repeat: matches 446. .513 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = "MLT1J repeat: matches 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="MLT1J repeat: matches 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ="LTR16C repeat: matches 199.
  "FAM repeat: matches 122.
.20282
                                                                                                                                                                                                                                                                                                                                                                                                                                      "AluJb repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "AluJo repeat: matches 1. .300 of consensus"
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                                                                                                                                                                                                                             15816
                                                                                                                                                                                                                                                                                                                        JIID repeat: matches 1.
.2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ME1 repeat: matches 4507. .5177 of consensus
                                                                                                             repeat: matches 2644.
                                                                                                                                                                                                   repeat: matches 2599.
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                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 3855.
                                                                repeat: matches 5522.
                                                                                                                                                        repeat: matches 18.
                                                                                                                                                                                                                                                repeat: matches 4477.
                                                                                                                                                                                                                                                                                              repeat: matches 2245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 1.
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                                                                                                             .2708 of
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30. .21954
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                         matches 5191. .6144 of consensus
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              Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                    Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de.mayer@mips.biochem.mpg de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales; Brassicacea 1 (bases 29277 to 29787; 37368 to 37886)
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EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                         Bevan, M., Rose, M., Hempel, S., Vos, P., Mewes, H.W., Lemcke, K.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                     E-mail: michael.bevan@bbsrc.ac.uk
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                                                                                                                                                                                                                                                                                                                Mayer,K.F.X.
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Heijnen, L., Vos, P., Mewes, H.V
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50769. .50927
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/note="L1MC1_repeat: matches 5682.
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1097. .51252
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Mewes,H.W., Lemcke,K. and
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BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2710 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .262 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone
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                                                                                                                                                                                                                                                 Jesse,T., Heijnen,L.
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18128. 18268,18591. 18613,18688.
19910. 20110,20250. 20399,20515.
21161. 21229,21319. 21624,21715.
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/gene="AT4g35790"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="overlap to
EMBL:AL031135 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similarity to phospholipase D, Arabidopsis thaliana, gb:U84568 contains EST gb:A1993659.1, W43871, W43825, H3631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(16756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
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                                                                                                                          complement(18128.
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                                                                                                                                                                               complement(18016.
                                                                                                                                                                                                              complement (17992.
/gene="AT4g35790"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="AT4g35790"
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                                                                                           complement(18269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="putative protein"
'protein_id="CAA21465.1"
         complement(18614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WDEKFNISIAHPFAYLEFQVKDDDVFGAQIIGTAKIPVRDIASGERISGWFPVLGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \CARPTDTDDVDPRDKGEFGDKNIRSHRKVITSDPYVTVVVPQATLARTRVLKNSQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
                                                                            /number=4
                                                                                                                                                                  number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAEKVSEDVMLLHGDLDLKIVKARRLPNMDMFSEHLRRLFTACK
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LCDGRYDTPEHRILHDLDTVFKDDFHNQDDALIRIGNILSVTLEFVFELKDGTS
NFEQRWINGATRWKEFSLERLKGKTHWQDDALIRIGNILSVAFELKDGTS
PCVWVSKEDDEBRWHVQIFRSIDSGSVKGFPKYEDDEARAVHLECAKRLVDK
IQTIRSAQHFIYIENQYFLGSSYAWBSYRDAGADNLIPMELALKIVSKIRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGVRVLLLVWDDKTSHDKFGIKTPGVMGTHDEETRKFFKHSSV
FKQQASPSSSIYIMTVVGTLFTHHQKCVLVDTQAVGNNRKVTA
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          .18687)
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d annotation"
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.18784,19341. .19.
.20663,20872. .29.
.21909,22187. .29.
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	- CDS	exon	gene	gene	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon
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b:S11960 gene contains ich is present in simil iffers at position 2952 etch has been verified	467824846,2495325024,25138. 2029006,2910129436,295222 4130202,3028830446,305243	.24846)		1678. 24846.24953. 25024.25138. 20. 29006,29101. 29436,29522. 2 41. 30202,30288. 30446,30524. 3 72. 31455))	. 23438)	.22496)	. 22336)	.22186)	.21909)	.21714)	.21624)	.21318)	. 21229)	.21160)	.21019)	.20871)	. 20663)	.20514)	. 20399)	.20249)	.20110)	:19909)	.19633)	.19340)	.18784)
an intron at lar proteins 20-29525 from on BAC	13828199, 229663, 430808,			138. 28199, 2. 29663, 4. 30808,		•					•														
	exon	gene	i Contraction of the Contraction	FEATURES	ĀĽ			REFERENCE		SOURCE	Z	ITION	RESULT 39 ATT19K4	DD /2342 AA	788	Matches '	Query Match				_				
				Coordi Labora E-mail	Submit: Biocher	i a	Vos, P. Unpubl	1 (ba:	Eukaryo Sperma Rosida	thale	AL0223	Arabid	ATT19K	MACGAA	AAAACGAA	121; C	ъ Т								٠.

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ATGGAAAAGGAATC 72562 •
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Conservative 0;
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RNA polymerase II heptapeptide repeat
AA1685-1691;Eukaryotic RNA polymerase II heptapeptide
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II heptapeptide repeat AA1636-1642;Eukaryotic RNA
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; Pred. No.
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yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; atophyta; Magnoliophyta; eudicotyledons; core eudicots; ae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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., Wedler, H., Wambutt, R., Hoheisel, J., Jesse, T., Heijnen, L., Mewes, H.W., Mayer, K. and Schueller, C.
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clone T19K4 (ESSAII
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tted (07-APR 1998) MIPS, at the Max-Planck-Institut fuer lemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: slle@mips.biochem.mpg.de or mayer@mips.biochem.mpg.de Project linator: Mike Bevan, Molecular Genetics Department, Cambridge ratory, John Innes Centre, Colney Lane, NR4 70J Norwich, UK, atory, John Innes Centre, l: michael.bevan@bbsrc.ac. abidopsis sequencing, project. t Submission

ses 1 to 106007)

ished

/note="strong similarity to predicted protein A\_TM017A05.8
of Arabidopsis thaliana BAC TM017A05, Patchx:G2435517 join(285. .374,483. .718,803. .1027,1117. .1252,1351. .1412, 1870. .1904,1987. .2210) /genem\_T19K4.10" /db\_xref="taxon:3702" /chromosome="4" 285. .2210 /organism="Arabidopsis /variety="Columbia" /number=1 /gene="T19K4.10" /gene="T19K4.10" ocation/Qualifiers thaliana"

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/prodein_id="Caal8483.1" /protein_id="Caal8483.1" /db_xref="Gi:3036793" /db_xref="Sp!trembl:065626" /db_xref="Sp!trembl:065626" /db_xref="Sp!trembl:065626" /db_xref="Sp!trembl:065626" /ctanslation="MASATSNNPASSSMSPRISGNHGSPTASVAQSPRRPSRQVSSP /translation="MASATSNNPASSSMSPIEPIASVSYAAPTAAVLTVEAAAGDEKSE MTQIVVRGESEPIAAAAAVAQPSSPQSRAPIEPIASVSYVAAPTAAVLTVEAAAAGDEKSE ASGGDNAGKKPVWKRPSNGASEVGPVMGASSWPALSETTKAPSNKSSDSLKSLGDV PSSSSASSSYPVTQGIANASVPAPKQAGRANPNPTPNHSQQRSFKQRAGSGSANCTV SQSSASSSSYPVTQGIANASVPAPKQAGASQNHGGTENSQRDSYRQNCHHQSHGG PSSSASGSVETEPSHNSPRGQNGVNGFASQNHGGTENSQRDSYRQNAAQPFPSHIP RRNQEHGNQNWTFQRSFNGREGNAQSQRGTPAFVRHPSPTVQPIPQFMAAQPFPSHIP FPTDIYLRGFMNNEGGFVPLRVVAGFKKVAELTDNIQQIVEALQNSPHVEVQGDFIRKR	protein coded for by gene T12F5.5 in ins cosmid T12F5, Patchx:G2773235	4443,49175406,57395809,63216392,	20"	0 9K4 . 10"	number=6 905. 1986 gene=TT19K4.10"	4131869 'gene="T19K4.10" 'mumber=5 8701904 'gene="T19K4.10"	וו כו וו כ	/umber=3 /117. 1252 /gene="T19K4.10" /number=4	/gene="T19K4.10" /number=3 1028. 1116 /gene="T19K4.10"	/gene="T19K4.10" /gene="T19K4.10" /number=2 803. 1027	/Humber - 1 483. 718 /gene="T19K4.10" /number = 2 710 803	375482 /gene="T19K4.10"	/LTANSIATLON="WVALDIGSDLFWVPCDCGKCAPTEGATYASEFELSIYNPKYSTY /KKYTCNNSLCAQRNQCLGTFSTCPYMVSYVSAQTSTGGILMEDVMHLTTEDKNPERV EAYVTFGCGQVQSGSFLDIAAPNGLFEGLGMEKISVPSYLAREGLVADSFSMCFGHDGV GRISFGDKGSSDQEETPFNLNPSHPNYNITVTRVRVGTTLIDDEFTALFDTGTSFTYL VDPMYTTVSESAQDKRHSPDSRIPFEYCYDMREKLVLAMKKFDCYDIEETNTTVAGTN KTAAVAPAMAAGIKTHNNSSELHKTNQTISKSNSSPNQISKTVDVWSFFRRVFILLPL VT	Contains eukaryotic and viral asparty] proteases active sites [VALDTGSDLFWV] and [ALFDTGTSFTYL]" /codon_start=1 /product="putative protein (fragment)" /protein_id="CAA18482.1" /db_xref="GI:3036792" /db_xref="SPTREMBL:065625"
	•			,									,	
		CDS	gene	gene exon	exon		•		gene	exon	exon	intron	intron	intron

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DNWQNWVLRRNPTGSGPQSVDRADAVAKRLGNLSVDQSSADPIGGSSSQLQPTEALSD
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ne="T19K4.40"
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sclspfakdlhvvpvesifgsdsldaadrllkildsvpddygkeddllhiknisl
aaengynrlvlgsctsriashvltavtvkgrgyslsadiqhvdarwkvpivlflrd
                                                                                                                  oduct="putative protein"
otein_id="CAA18485.1"
_xref="GI:3036795"
                                                                                                                                                                                          Le="similarity to predicted protein F29F11.3,
norhabditis elegans, Patchx:E248390
ains EST gb:T21369"
                                                                                                                                                                                                                                                                       olement(join(14550. .14672,14834. .14891,15525. .15919,
20. .16158,16200. .16321,16597. .16683,16777. .17140,
20. .17503))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ıber=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nber=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nber=2
                                                                                                                                                                                                                                                           e="T19K4.40"
                                                                                                                                                                                                                                                                                                                                          e="T19K4.40"
                                                                                                                                                                                                                                                                                                                                                             ilement(join(14550...14672,14834...14891,15525...15919,
:0...16158,16200...16321,16597...16683,16777...17140,
:8...17503))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lon_start=1
douct="putative bZIP transcription factor"
)tein_id="GAN18484.1"
_xref="GI:3036794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ains bZIP transcription factors basic domain signature {\tt IIKNRESAARSRAR},"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le="T19K4.30"
e="weak similarity to GBF4, Arabidopsis thaliana,
f:G403418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i. .6899
ne="T19K4.20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="T19K4.20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e = "T19K4.20"
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e="T19K4.30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ber=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NRESAARSRARKQECASPLPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .17503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5809
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VERSION
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AC008034/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15469 AAAACGAATGGAAAAGGAATC 15489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oyudon,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Shoshtari,N., Scherer,S., Soutt,G., Shon,H., Shoshtari,N., Cotton, S., Savery,G., Scherer,S., Soutt,G., Shon,H., Shoshtari,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Al
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Bari
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J
               Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Pr
1 (bases 1 to 120134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC008034.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC008034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burch, P., Burkett, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTGS_PHASE1; HTGS_DRAFT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(15525.
/gene="T19K4.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(14834. .14891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(14673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMISQVKHQKVDSQAYLRHYNTKRLMFDQFIKSDGRMGRFAFLLKKSKTIAQRRSILP
EIGKKEKVRRELKIKALEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt CVRLEITRLCLLDGEPYSCIIQLLSDVTYSGQGRLKTVELACRSQCGINDLVSSFVAL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(14892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCPICNGPLNRSDSSELDTFEEGQESDVLYAACCSSCRFQILPQDGSSLEQFSSFLPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="T19K4.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavazos, S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120134 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB
s; Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burrell, K.L., Byrd, N.C., Carron, T.F.,
L., Chacko, J., Chavez, D., Chen, G., Chen, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VA HTG 17-JUL-2001 Clone CTB-134A23, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTGS_FULLTOP; HTGS_ACTIVEFIN
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17;
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                                        Tamerisa, K.
Vinson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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KEYWORDS
                                         VERSION
                                                                              ACCESSION
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                               99470 CTGTGGCAGCGGCGGCGGCAG 99450
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HTG.

Label 100 DNA PRI 20-JUL-200 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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DOE Joint Genome Institute and Stanford Human Genome Center
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On Jul 20, 2001 this sequence version replaced gi:13677003
Draft Sequence Produced by DOE Joint Genome Institute
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Quality: Phrap Quality >=40 99.7% of Sequence;
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Submitted (31-MAY-2001) DOE Joint Genome Institute, 2800 M: Drive, Walnut Creek, CA 94598, USA on May 31, 2001 this sequence version replaced g1:13676952. Draft Sequence Produced by DOE Joint Genome Institute
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Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-AUG-1997) Chromosome 13 Project Group (http://www.sanger.ac.uk/HGP/Chr13/) Sanger Centre, Hinxton, (cambridgeshire, CB10 15A, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on May 14, 2001 this sequence version replaced gi:1869765
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                                                                                                                                                                                                                                                                                                                       This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13q12-q13; CpG island
                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs human chromosome 13, constructed by the Sanger Centre chromosome mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McMurray, A. and Odell, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                      only a small overlap as described above.
179115 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
                                                                                                            together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with
                                                                                                                                                                                                                              The true left end of clone 179115 is at 1 in this true right end of clone 49J10 is at 54668. The true left end of clone 46H23 is at 146707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone 179115 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                        corresponding to the overlapping clone as only a small overlap as described above.
                                                                                                                                                                                    During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45816
                                                                                                                                                                                                                                                                                                        feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3q12-q13 contains Klotho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 146810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z92541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CTC-426L22"
29494 c 29282 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:2370068
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146810 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29282 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179115,
STs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrată; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRCA2 gene
CpG island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 143661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region chromosome
                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-1999
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source

55591	repeat_region				B repear. marcines	repeat_region 23	rep
54190	unsure					repeat_region 22	rep
53734 /note	repeat_region		_		matches 51223	repeat_region 22 /r	rep
53125 /note	repeat_region				/note="AluSq repeat: matches 1301 of consensus"	repeat_region /r	rep
/note	- 1				Ŋ.	1, 0, 10	1
/note	reneat region				Ä	region 2	ren .
/note 50360	repeat_region				<pre>/note="MIR repeat: matches 13335 of consensus" 1734017639</pre>	/r repeat_region 17	rep
/note	repeat_region				at: matches 3651 o	repeat_region 16	rep
48988	repeat_region					repeat_region 15	rep
48909 /note	repeat_region				.14366 MLT1D repeat: matches 500 2 of	repeat_region 13 /r	rep
44988 /note	- unsure				.13774 AluSx repeat: matches 1298 of	repeat_region 13 /r	rep
44935 /note	repeat_region				239512604 note="MIR repeat: matches 22218 of consensus"	repeat_region 12 /r	rep
44193 /note	repeat_region	-			3.		rep
42420 /note	repeat_region				data only"	unsure 11	uns
41740 /note	repeat_region				102211364 note="MLT1B repeat: matches 67390 of consensus"	repeat_region ii	rep
/note	Tebeac_TeATON						,
/note	1				~	٠,	j .
/note 40770	repeat region			,	/note="MLT1C repeat: matches 186 of consensus" 1035411007	/r repeat_region 10	rep
40435	repeat_region				6 The sor of the sort of the s	repeat_region 10	rep
40086	repeat_region				200	repeat_region 95	rep
39536 /note	repeat_region	-			ᄗᇻ	L. <b>.</b>	
39384 /note	repeat_region				/note="2 copies of 56 mer 84 % conserved" 93109576	/n repeat_region 93	rep
39109 /note	repeat_region		•		/note="11 copies of 2 mer 100 % conserved" 9168. 9279	/n repeat_region 91	rep
/note	repeat_region				OILLY	repeat_region 82	rep
/note	5				.7255	. ~1.	unsure
/note	repeat region				/note="15 copies of 2 mer 93 % conserved"	repeat_region 60 /n	rep
/note	repeat_region				57275897 /note="MER42B repeat: matches 11091300 of consensus"	repeat_region 57	rep
32875	unsure				USUS		
31268	repeat_region					epeat_region 52	rep
31050	unsure				note="MLT2_internal repeat: matches 31462693 of	u/ u/ iorforthada	4
30925	repeat_region					٠.٠	5
30635 /note	repeat_region				3808	epeat_region 38	rep
29067	repeat_region				3 II.	· ·	ļ
28700	repeat_region					repeat region 36	T PD
28600 /note	repeat_region	. "			matches 30	repeat_region 33 /n	rep
28240 /note	repeat_region				7781945 "note="3 copies of 56 mer 85 % conserved"	repeat_region 17 /n	rep
incom)	_				note="AluJo repeat: matches 2962 of consensus"	<u>_</u> +	dər
/note 26939	repeat_region				9 6		
26810	repeat_region			٠,	map=113(12-q13)	/m	
25654	repeat_region			٠.	db_xrrf="taxon: 9606"		
/note:		_	_		rapiem="Homo excione"	· /o	

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.e="AluJo repeat: matches 130. .1 of consensus
implete repeat"
0. .28439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="L1ME3A repeat: matches 585. .366 of consensus"
0. .26857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="MLTIG repeat: matches 160. .31 of consensus"
4. .25859
e="49J10 data only"
1; .56086
                                                  e="MIR2 repeat: matches 25. .146 of consensus"
                                                                           e="AluSg repeat: matches 1.
4. .53853
                                                                                                                 e="MER5A repeat: matches 103. .7 of consensus" 5. .53426
                                                                                                                                                             e="MIR repeat: matches 18. .228 of consensus"
8. .53072 ·
                                                                                                                                                                                                                                          e="L1PB1 repeat: matches 901.
5, .49871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="MLT1A2 repeat: matches 374. .1 of consensus"
7. .29208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="MIR repeat: matches 261. .159 of consensus"
                                                                                                                                                                                                                                                                              e="MIR2 repeat: matches 144.
8. .49571
                                                                                                                                                                                                                                                                                                                                                                                                                                               e="MLT1D repeat: matches 1.
3. .45080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y="AluJo repeat: matches 1. .302 of consensus"
). .41372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ""L1ME1 repeat: matches 915. .540 of consensus"
. .40231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "AluJb repeat: matches 296. .1 of consensus"
.42353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "MIR repeat: matches 47. .207 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "AluJo repeat: matches 5. .38586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "49J10 data only"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "MER34 repeat: matches 267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 copies of 2 mer 81 % conserved" .27058
                                                                                                                                                                                                                                                                                                                                                                                                     L1PA2 repeat: matches 893. .1 of consensus"
.45858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MER34 repeat: matches 532.
.31199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ll repeat: matches 4313. .3694 of consensus"
.42917
                                                                                                                                                                                                                   'SLRNA repeat: matches 258. .314 of consensus"
                                                                                                                                                                                                                                                                                                                        19J10 data only"
.48964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMD2 repeat: matches 744. .2 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIR repeat: matches 162. .15 of consensus"
30919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IR repeat: matches 223.
28699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l repeat: matches 5013. .4394 of consensus"
41728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luJo repeat: matches 293. .1 of consensus 37341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9J10 data only"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ık repeat: matches 88.
39270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4333
                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 5390. .4467 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 5390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 repeat: matches 70. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .302 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .20 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5107 of consensus
                                                                                            .300 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .503 of consensus"
                                                                                                                                                                                                                                                                                                     .88 of consensus"
                                                                                                                                                                                                                                                           .269 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .255 of consensus
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RESULT 4
AC068315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73954 AAGCAGTTGTCATTTGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1175 AAGCAGTTGTCATTTGGAAGT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
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                    Sequencing vector: pUC18; 100% of reads
Chemistry: Dye terminator: ET 55% of reads
Chemistry: Dye terminator Big Dye; 45% of reads
Chemistry: Dye terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 154843 bases at least Q40
Consensus quality: 156911 bases at least Q30
Consensus quality: 168985 bases at least Q20
Insert size: 139544; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
SEQUENCE, 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-MAY-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, 100101, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bao, W., Hu,S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, O., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Ot, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.
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Quality coverage:
                                                                                                                                                                                                                                                                                                                            Center clone name: RP11-224P21
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center:Beijing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 27, 2000 this sequence version replaced gi:8101156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Yang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromosome 3p genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu.S., Li.T., Liu,Y., Liu,N., Liu,B., Liu,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M. Tao,R., Wang,H., Wang,J., Wang,L., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F. Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,Thang,L., Zhang,M., Zhang,X., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Website:http://hgc.igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code:Beijing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 155313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 to 155313)
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.36x in Q20 bases; sum-of-contigs
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3 clone RP11-224P21 map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, X., Zhang, Y., Zhang, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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3p, WORKING DRAFT
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H., Zhang, H.,
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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/note="assembly\_name:Contig32"

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Li,J.,

, Li,L., , Li,Y., Sun,Y.,

He, L.,

Hu,S.,

Chen, J., Ding, H.

Xuan, Zhang, Y.,

Zhang,H.,

Beijing, Beijing

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BASE COUNT
ORIGIN
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AC066599
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       DEFINITION
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AC066599 157007 bp DNA HTG 19-SEP-2000 HOMO sapiens chromosome 3 clone RP11-596J9 map 3p, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ="assembly_name:Contig42"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 150014 bases at least Q40 Consensus quality: 153515 bases at least Q30 Consensus quality: 155718 bases at least Q20 Insert size: 149003; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: pUC18: 100% of reads Chemistry: Dye-terminator: ET 55% of reads Chemistry: Dye-terminator Big Dye; 45% of reads Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-APR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing 100101, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, J., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, C., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Li, G., Chang, F., Zhang, C., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J., Hang, Y., Li, L., Feng, X., Yu, J., Hang, M., Li, L., Hang, M., Li, L., Feng, X., Yu, J., Hang, M., Li, L., Hang, M., Ha
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Center code:Beijing
Website:http://hgc.igtp.ac.cn
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On Sep 19, 2000 this sequence version replaced gi:8101249
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Mammalia; Eutheria; Pr
1 (bases 1 to 157007)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: 1% project Center clone name: RP11-596J9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Yan,C., Yang,X., Yu,B., Zeng,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang,L., Zhang,M., Zhang,X., Zhang
Zhang,Z., Zhu,B., Yu,J. and Yang,H.
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                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                              be preserved
                                                                                                                                                                                                                                                                                                                        as soon as it is available and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 157007)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Wang, H., Wang,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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., Kang, N., Li, C., Li, C.
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Search completed: March 29, 2002, 21:43:28 Job time: 6623 sec
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/db_xref="taxon:9606"
/chromosome="3"
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17988. .157007
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)6. .117887
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## ALIGNMENTS

AAZ23249 RESULT

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AAZ23249 standard; cDNA; 1275 BP

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XXX XX DE Hillman JL, Hawkins PR; (INCT-) INCTYE PHARM INC 31-OCT-1996; 13-AUG-1998; 09-NOV-1999 US5981232-A. Homo sapiens Human; pyrophosphatase; HPYP; genetic engineering; inflammatory disease; cancer; diagnostic assay; ss. Human pyrophosphatase (HPYP) encoding cDNA 24-JAN-2000 (first entry) 96US-0741437 98US-0134593

Human gene signatu

Disclosure; Fig 1A-D; 30pp; English

Human pyrophosphatase used in treatment and prevention of cancer

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Query Match
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Matches 1275; Conserv
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Human; inorganic pyrophosphatase; HPYP; Incyte clone 768320; cell regeneration; tissue regeneration; ss.
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             DNA encoding human pyrophosphatase protein recombinant protein, which may be useful in protein.
                                                                                                          Hawkins
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tissue regeneration
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                                                                                                                                       (INCY-) INCYTE PHARM INC
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                                                 gactaagaaaacgaatggaaaaggaatcagttgcatgaatacaactttgtctgagagccc
                                                            GACTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCC
                                                                                                   agataaggactttgccattgatattattaaaagcactcatgaccattggaaagcattagt
                                                                                                                AGATAAGGACTTTGCCATTGATATTAAAAGCACTCATGACCATTGGAAAGCATTAGT
                                                                                                                                                       aaggtataaggttcctgatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261
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immunosuppressive; antianaemic; antiasthmatic; antia
antirheumatic; antiathritic; inflammatory disease;
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polynucleotides,
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bone marrow, prostate tissue and could involve supplying various natural molecules, in drug regimes that allow cell division and differentiation to occur. The polynucleotides may be used to detect quantify gene expression in biopsied tissues in which expression of HPYP may be correlated with a disease, for screening libraries of
HPYP may be correlated with a disease, for screening libraries of compounds in various drug screening techniques, and in molecular biology techniques. Vectors expressing antisense and antagonists or inhibitors of the protein may be used to suppress the excessive proliferation of inflammatory cells which cause damage in immunological disease.
                                                                                                                                                                                                                                                                                                                                in the diagnosis, prevention and treatment of inflammatory giseases a cancer. HPYP and the vector encoding HPYP may be used to in the regeneration or transplantation and development of nerve, pancreatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing, preventing and or in screening libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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of compounds for various drug screening
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Sequence 394 A; 235 Ç; 294 G; 351 T; 3 other; myasthenia gravis, diabetes mellitus, osteoporosis, glomerulonephritis rheumatoid and osteoarthritis, and scleroderma. The present sequence represents the coding sequence of human pyrophosphatase.

diseases, such as anaemia, asthma, systemic lupus erythematosus,

Query Match Best Local

Similarity

DВ

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                                                                                                                     TATCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAG
                        aaccgactggaaagtcattgccattaatgtggatgatcctgatgcagccaattataatga
                                                                       aagaggtgaaataattggcgtgaaagttctaggcatattggctatgattgacgaagggga
                                                                                  AAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAÁGGGGA
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                                                                                                                    ACTAAGATAACTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTT
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                                                                                                          actaagataacttttagcacatgcttaaatatcaaagcagttgtcattttggaagtcactt
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RESULT
AAX00685
 AAX00685
standard; DNA; 1351
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25-MAR-1999

(first entry) protein

gene 75

clone HOSEI45

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymous; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption;

01-OCT-1998 W09842738-A1

Homo sapiens

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                                                                                                                                                                                  Query Match 95.2
Best Local Similarity 99.9
Matches 1264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW07807-W688004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological
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Greene JM,
                                                                                                                                                                                                                                                                                                                conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expresse polynucleotides, based on which tissues they are most highly expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 233-234; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-070066/06.
P-PSDB; AAW67881.
                                                                                                                                                                                                                                                                 Sequence 1351 BP; 414 A; 252 C; 319 G; 362 T; 4 other;
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                                                                 20 ggggctctctcccttgtcagtcggcgccgcgtgcgggctggtggctctgtggcagcggcgg
                                                                                                                                 Ruben SM,
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Hu JS, Lafleur DW, Moore PA,
Ruben SM, Shi Y, Young P;
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                                                                                                                                                                                  Score 1214; DI
Pred. No. 0;
0; Mismatches
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Ni J, Olsen HS;
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for each of the 87
highly expressed
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CAAGGGGAGCACATATTGGATGTATATGTTACCATATGTTAGGAAATAAAATTATTT 	CTTTTAGCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGAT	AATCCAATATACTCAGAATGTTATCCATCTAAAGCATTTTTCATATCTCAACTAAGATAA 	AGCTTTTCAAAGCTTTAAATTTGTAGAACTCATCTAACTAA	AATACAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGT 	AAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCT 	TCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCCTGTGAATCTGCCTGC	CCCCTTCAAGTGT              ccccttcaagtgt	AAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAA 	TCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTTAAAGATAAGGAC 	TCAAACGGTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAG 	AAGTCATTGCCATTAATGTGGATGATCCTGATGCAGCCAATTATAATGATATCAATGAT	AATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAACCGACTGG 	TGACAATGACCCAATTGATGTGTGTGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAA 	TGCCATCCCTCAGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGGCTGTTGT 	AGGAAAACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTAT 	AATGCAAAATGGAGATTGCTACAAAGGACCCTTTAAACCCTATTAAACAAGATGTGAAA	TCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCT 	gagaaaggacaatatatatctccatttcatgat
1270 1279	1210 1219	1150	1090	1030	970 979	910 919	850 859	790 799	730 739	57		550 559	490 499	430 439	370 379	310 319	250 259	199

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RESULT
AAX00716
      CCC XXX PT PT CCC CCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX00716 standard;
    This sequence represents secreted human protein.
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                                                                            New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                    Claim
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DB; AAW67912.
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Lafleur D
M, Shi Y,
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The gene number,
        nucleic acid molecule which encodes he gene number, and the clone it is
                                                                                                                                                                                            R, Ferrie AM,
DW, Moore PA
Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 clone HOSEI45
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generate fusion proteins by linking to the gene to a hun FC portion (e.g. AAX00602) for increasing the stability protein as compared to the human protein only. The invention relates to 87 novel genes and their fragme acid sequences: AAX00611-V0077.
                                                                 conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed
                                                                                                                                                                                    The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical
Sequence 1350 BP; 414 A; 250 C;
                                           (see AAX00611
                                                for described uses).
    319 G;
    363 T;
                                                                                                                                                                   Also, pathological
       4 other
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Query Match Best Local

Score 1153;
· Pred. · No.

0; ВG 20;

Length 1350;

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В Qy DЬ Qy В Ωy Вþ Ωy Ş Qy Дb ν Q В ρy В Qy 밁 밁 Š 밁 Ωy g Best Local Similarity Matches 1153; Conserv 791 731 723 671 663 611 603 551 543 491 483 431 423 371 363 311 303 251 243 191 183 783 ATAAGGACTTTGCCATTGATATTAATTAAAAGCACTCATGACCATTGGAAAGCATTAGTGA TCAATGATGTCAAACGGCTGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAA ccgactggaaagtcattgccattaatgtggatgatcctgatgcagccaattataatgata CCGACTGGAAAGTCATTGCCATTAATGTGGATGATGATGCAGCCAATTATAATGATA 602 gaggtgaaataattggcgtgaaagttctaggcatattggctatgattgacgaaggggaaa GAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGATTGACGAAGGGGAAA atgtgaaaaaaggaaaacttcgctatgttgcgaatttgttcccgtataaaggatatatct ATGTGAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCT gctggtctaatgcaaaatggagattgctacaaaggaccctttaaaccctattaaacaag GCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAAACCCCTATTAAACAAG ttcatgatattccaatttatgcagataaggatgtgtttcacatggtagttgaagtaccac TTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTAGTACCAC CTAAGAAAACGAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCT ggtataaggttcctgatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaaag GGTATAAGGTTCCTGATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAG tcaatgatgtcaaacggctgaaacctggctacttagaagctactgtggactggtttagaa TCAAGTGTGATCCTGATGCTGCCAGAGCCATTGTGGATGCTTTACCACCACCCTGTGAAT ctaagaaaacgaatggaaaaggaatcagttgcatgaatacaactttgtctgagagcccct 90.4%; llarity 100.0%; Conservative 0, Mismatches 0; Indels 0; Gaps 302 542 310 190 662 550 490 482 250 842 782 722 670 610 850 790 730 902

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antitumor activity. Polypeptides (I) encoded by (A) are used: (i) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise
                                                     This invention describes novel nucleic acid sequences (A) that a expressed at high level in prostatic tumor tissue and encode generoducts or their fragments. The products of the invention have
                                                                                                   Claim
                                                                                                                       encoded polypeptides, therapeutic agents -
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                                                                                                    1a;
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                                                                                                                                              acid expressed
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                            CC of the invention can be used for gene therapy. (A) are used (1) for CC recombinant expression of polypeptides (B) and (ii) to isolate complete CC genes. (B) are used (i) to identify agents suitable for treatment of CC ovarian cancer; (ii) directly for treating this form of cancer (c) including expression from gene therapy vectors) and (iii) for generation CC of specific antibodies. (A) are identified by assembling ESTs (expressed CC expression patterns. This allows a significantly longer fragment of the CC expression patterns. This allows a significantly longer fragment of the CC gene to be revealed, so should reduce the number of fallures associated CC with the fact that ESTs from different libraries may represent different CC parts of the same unknown gene, distorting the estimated frequency of CC occurrence in a particular tissue. AAZT/450-27/572 represent the human CC ovarian tumor cDNA library derived EST fragments described in the method CC of the invention and encode the protein fragments represented in
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(first entry)

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Best Local S
Matches 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs: 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping prodices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                      CCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCTGGAATA
                                                                                                                                                                                                                                                         attgatattattaaaagcactcatgaccattggaaagcattagtgactaagaaaacgaat
                                                                                                                                                                                                           GGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCTTCAAGTGTGATCCT
                                                                                                                                                                                                                                                                                                               gatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaaagataaggactttgcc
                                                                                                                                                                                                                                                                                                                             GATGGAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACTTTGCCC
TCAAAGCTTTAAATTTGTAGAACTCATCTAAACTAAAGTAAAATTCTGCTGACTAATCCA 109
                        ggaaaaggaatcagttgcatgaatacaactttgtctgagagccccttcaagtgtgatcct
                                                                                                                                                                                                                                                                      ATTGATATTAATAAAGCACTCATGACCATTGGAAAGCATTAGTGACTAAGAAAACGAAT
                                                   CAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGCTTT
                                                                             ccaacagacgtggataagtggttccatcaccagaaaaactaatgagatttctctggaata
                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one of a large number of 5' ESTs derived
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                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
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                          polypeptide can then be used to inhibit cancer development. CD4+ and/or CD8+ T-cells from a patient may be incubated with a polypeptide or nucleic acid of the invention, or an APC expressing such a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be cloned and then administered back to the patient to inhibit cancer
                                                                                                           portions of proteins which are associated with human colon tumours. The invention also specifically discloses 8 human colon tumour proteins (AABI1897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, especially colon tumour cells, thereby inhibiting the development of cancer. T-cells specific for the polypeptide expressed by the APC are used to, remove tumour cells from biological samples, especially blood or fractions thereof. The sample or the isolated T-cells specific for the
                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                 progression of the cancer
                                                                                                                                                                                                                                                                                                                                                                 especially colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              New colon tumor polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACATGCTTAAATATCAAAGCAGTTGTCATTTGGAAGTCACTTGTGAATAGATGTGCAA 1216
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                                                                                                                                                                                                                                                                                                               Page 212;
                                                                                                                                                                                                                                                                          AAA77722-A78199 represent 478 cDNAs encoding proteins or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human colon tumour polypeptide,
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99US-0401064.
99US-0444242.
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                                                                                                                                                                                                                                                                                                                                                                 cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secrist H,
                                                                                                                                                                                                                                                                                                              229pp; English
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encoding the polypeptides and antibodies ay be used to determine the expression le
                                                                                                                                                                                                                                                                                                                                                                used to inhibit the development of cancer for diagnosing and monitoring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; vaccine;
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monitor the progression of a cancer by repeating the processes at intervals, and comparing the current result to previous results. The present sequence represents a CDNA encoding a human colon tumour

are present. Such diagnostic methods may also

the invention,

and therefore to

determine whether be used

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of a tumour protein of cancer cells are presen

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AAI28873/c
ID AAI288
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                                       10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
                   29-JUN-2000;
28-AUG-2000;
                                                                                                                                                                                        Human; immunotherapy; diagramminogenic; gene therapy;
                                                                                                                                                                                                                        Colon tumour
                                                                                                                                                                                                                                                                AAI28873;
                                                                                                                                                                                                                                                                                    AAI28873 standard; cDNA;
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(CORI-)
                                                                                  30-DEC-1999;
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                                                                                                         29-DEC-2000;
                                                                                                                                                WO200149716-A2
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                            12-OCT-2001
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                                                                                                                            12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                 235 GAAAACCAGAAAATGAGTTTGCGTTTAATGCAGAATTTAAAGATAAGGACTTTGCCATTG
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nes 415; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCTGATG
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                      2000US-0575251.
2000US-0609448.
2000US-0649811.
                                                   2000US-0480321.
2000US-0504629.
2000US-0519444.
                                                                                                                                                                                                                        related
                                                                                                         2000WO-US35596
                                                                                    99US-0476296
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                                                                                                                                                                                                                        determined
                                                                                                                                                                                                    diagnosis; colon cancer; colon tumour;
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                                                                                                                                                                                                                                                                                     578
                                                                                                                                                                                                                                                                                      ₽P.
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                                                                                                                                                                                                                         for clone 31985
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116 800 176 740 236

56 860

Sequence

578

BP;

32.5%;

Score 415; DB 22; Pred. No. 6.5e-198;

Length

0;

155 A; 139 C; 99 G; 185 T; 0 other;

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ce expression; such as colonic cancer. For example, (1) and (11) may be used to treat disorders associated with decreased expression by creatifying mutations or deletions in a patient's genome that affect the creatifying mutations or deletions in a patient's genome that affect the creatifying mutations or deletions in a patient's genome that affect the creatifying mutations or them. Additionally, (1) may be used to patients own production of them. Additionally, (II) may be used to complements own production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic coll culturing the cell to express the protein (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic confictate the presence of Similar nucleic acids in samples, and complementate the presence of Similar nucleic acids in samples, and continue the presence of TCAP expression and activity. Cand in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate as diagnostic agents for detecting the presence of TCAPs in samples cand AAM2494 to AAM24523 represent nucleotide and amino acid sequences and in the promotification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with inappropriate colon tumour associated protein (TCAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                   exemplification of the present invention.
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. Jiang Y;
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                                                                                                                                                                                                                                                                                                                                                                                      different mRNAs in the particular tissue from which it was derived the appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene signature; messenger RNA; mRNA; relative abundance human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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(OKUB/) OKUBO K.
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GGAATACAAGCTGATATTGCTACATCGTGTTCATCTGGATGTATTAGAAGTAAAAGTAGT 1030
                                                                                                                                                   ACAGTACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAAACTAATGAGATTTCTCT
                                                                                                                                                                                    gatectgatgetgecagagecattgtggatgetttaceaceacectgtgaatetgeetge
                                       <u>ggaatacangctgatattgctacatcgtgttcatctggatgtattagaagtaaaagtagt</u>
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                                                    have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (1) for recombinant expression of polypeptides (B) and (il) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer covarian cancer; (ii) directly for treating this form of cancer of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ77450-Z7757 represent the human ovarian tumor cDNA library derived EST fragments described in the method
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                                                                                                                                                                                                                                                                                                             Claim 3; Page 157; 310pp; German.
                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
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                            of the invention and encode the protein AAY76505-Y76638.
                                                                                                                                                                                                                                                                                  This invention describes novel nucleic acid (cDNA) sequences
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                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA of the mRNA because they are often obtained from oligo-dT primed cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted
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                                               libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000;
                                                                                                                                                                                                                                                            Claim 1; SEQ
                                                                                                                                                                                                                                                                                        diagnostic,
                                                                                                                                                                                                                                                                                         obtaining cDNAs and ge diagnostic, forensic,
                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 ATTCCAATTTATGCAGATAAGG
                                          in diagnostic,
They are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCAGGACTCCGGCACTATGAGCGGCTTCAGCACCGAGGAGCGCGCCCCGCCCCTTCTCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attccaatttatgcagataagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' EST;
                                            used to obtain upstream regulatory sequences and
                             and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                          ID 19004; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed sequence chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%;
                                                                                                                                                                                                                                                                                           gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                      Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                              vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 202; DB
Pred. No. 3.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO: 19004
                                                                                                                                                                                                                                                                                                                                                                                        Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                             mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                for
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Sequence 121

BP;

41 A;

24 C;

26 G;

30 T; 0 other;

sequence tags (SESTs), isolated from human, mouse, chicken an tissue sources. The SESTs can have a range of activities depet the tissues they were isolated from. The activities include: chemotractic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinfla

antiinflammatory;

depending

g

ed expressed and rat

to AAA45925 represent specifically claimed secreted

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders

Claim 1; Page 738; 803pp; English.

WPI;

2000-317938/27

Jacobs K,

McCoy JM, Treacy M,

LaVallie Bowman

ER,

Collins-Racie

Evans

Merberg D,

(GEMY ) GENETICS INST

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RESULT 14
AAA45576
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Query Match
Best Local S
Matches 121
                                                                                                                                                                                                                                                                                                                                                                      lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA45576 standard; cDNA; 102
                                                                                                                                                                                                                                                                                                                                                                                                                               cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted expressed sequence tag SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombolytic; antiinflammatory; cytostatic; antibacterial;
                                                                                                                                                                                                                                                                                                                        WO200021991-A1
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 TAAACCCTATTAAACAAGATGTGAAAAAAAGGAAAACTTCGCTATGTTGCGAATTTGTTCC
                                                                                                                                                                                                                                               15-OCT-1998;
                                                                                                                                                                                                                                                                      15-OCT-1999;
                                                                                                                                                                                                                                                                                               20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 A 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunomodulatory; haematopoietic; chemokinetic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                taaaccctattaaacaagatgtgaaaaaaggaaaacttcgctatgttgcgaatttgttcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgtataaaggatatatctggaactatggtgccatccctcagacttgggaagacccagggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chicken; rat;
                                                                                                                                                                                                                                                98US-0104436
                                                                                                                                                                                                                                                                        99WO-US24206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 21;
Pred. No. 1.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO:2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), altergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45936 to AAA45931 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the SESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene
  Claim 25; SEQ
                          analyzing
                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                  30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                 WO200157278-A2
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                      Probe #12699
                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI22766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI22766 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiasthmatic; vulnerary; antiulcer; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                            04-OCT-2000;
                                                                                                                                                                    21-SEP-2000;
                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                  (MOLE-)
                                                                                                                                                                                                           26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 AATGATAAACATACTGGCTGTTGTGGGTGACAATGACCCCAATTGATGTGTGTAAAATTGGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AGCAAGGT 474
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                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agcaaggt 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                  MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
                          gene
                                                                                         Hanzel
                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial; antifungal; antiviral; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                2001WO-US00670
                                                                                                                                                       2000US-0234687
2000US-0236359
                                                                                                                                                                                2000US-0632366.
                                                                                                                                           2000GB-0024263.
  Ħ
                          expression
                                                                                         DK,
No 12699; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                      gene expression analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%;
100.0%;
                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
                          in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                          human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                         Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                      in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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expression in for antenatal

Claim analyzing

25; SEQ ID

No 16754; 654pp; English.

Human genome-derived single exon nucleic acid

gene expression

'n

human

placenta

probes useful

for

The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray, for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful

genetic

placenta. disorders

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RESULT 16
AAI48068/c
ID AAI48068 standard; DNA; 186
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WII
                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
                                                                                                                                                                                                          04-OCT-2000;
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27-SEP-2000;
                                                                                                                                                                                                                                            03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                       WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     genetic
                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #16754 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI48068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 186
                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to human single exon nucleic acid probes
                                                                                                                                 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTGG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 385
                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽₽;
                                                                                                                                                                                                                                                                                                        2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                          2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 A; 44 C; 33 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                      to measure gene expression in human placenta
                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66;
Pred. No.
                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 T; 0 other;
                                                                                                                                                         DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
4.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0

SX XX

Sequence 186

BP;

47

Α;

44 C;

ω Ψ <u>.</u>

62 T; 0 other;

Length 186;

밁 QΥ 밁

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RESULT 17
AAI08439/c
ID AAI08439 standard; E
XX
AC AAI08439;
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   22000x3
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Best Local (
                                                                                                               The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #8430 used
                                               non-carcinoma tumours.
Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                          Claim 25; SEQ ID No 8430; 322pp; English.
                                                                                                                                                                                                                                                                                                                  Novel single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 ACTTGG
                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                           in a
                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 ACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-SEP-2000;
                                                                                                    the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                           human breast
                                                                                                                                                                                                                                                                                                                                                             2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00661.
BP; 47 A; 44 C; 33 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast disease; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                                                           Chen W;
                                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66;; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                             probe used
                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; 1
4.5e-23;
                                                                                                                                                                                                                                                                                                                               to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development disorder;
                                                                                                                                                                                                                                                                                                                             measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-carcinoma
                                                      part of the printed directly from WIPO
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                                                                                                                                                                                                              the probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Sequence 186

QY

'326 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG

Matches Query Match Best Local

Similarity

5.2%; su 100.0%; P

Score 66; DB; Pred. No. 4.6

DB 22; 4.6e-23;

Length 411

Indels

0;

Gaps .

0;

385

Conservative

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RESULT · 18
AAI13542/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #3475 for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI13542 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI13542;
                                                         expression, the probes are therefore useful in grading and/or of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                     Claim 25;
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 385
Sequence 411 BP; 106 A; 101 C; 67 G; 137 T; 0 other:
                                                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386
                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )3-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 5.2%;
1 Similarity 100.0%;
66; Conservative
                                                                                                                                                                                                                                                                     SEQ ID No 3475; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; I
. 4.5e-23;
ches. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                      part of the printed directly from WIPO
                                                                                                                                 staging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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RESULT 20
AAI03431/c
ID AAI03431 standard; DNA; 411 BP
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AAI34904/c
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI34904 standard; DNA; 411 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID No 3590; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI34904;
                                                                                                                                                                                                                                                                                                                    Sequence 411 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #3590 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
                                                                                        298
                                                                                                            386 ACTTGG 391
                                                                                                                                                                                           326 TATGTTGCGAATTTGTTCCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 ACTTGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386.ACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358
                                                                                                                                                          358 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTGG
                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391
                                                                                        293
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                    106 A; 101 C;
                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  placenta;
                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                            Score 66; DB 22;
Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                                                                  67 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                    137 T; 0 other;
                                                                                                                                                                                                                                                              Length 411
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                            0;,
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                       AAH35811
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the beast cancer, disorders of development, inflammatory diseases of the beast cancer, disorders of development, inflammatory diseases of the beast cancer, disorders of development, inflammatory diseases of the beast cancer, disorders of development.
                                                                                                                                                                                                                                                                                                                                                                                                                         of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the prinspecification, but was obtained in electronic format directly from W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-OCT-2001 · (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI03431;
                  AAH35811;
                                                   AAH35811 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 BP; 106 A; 101 C; 67 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY:2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; development disorder; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #3422 used to measure gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2000;
                                                                                                                                                                                                             -358 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG
                                                                                                                                                                                                                             326 TATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAG 385
                                                                                                                                           298
                                                                                                                                                                          386 ACTTGG 391
                                                                                    21
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                         ACTTGG
                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 3422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK, Chen W,
                                                                                                                                         293
                                                                                                                                                                                                                                                                                 larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312
2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0608408
2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000GB-0024263
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2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probe used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferative breast disease; non-carcinoma tumour.
                                                     342 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322pp;
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                               Score 66; DB; Pred. No. 4.6
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English.

measuring

gene

expression

the probe

DB 22; I 4.6e-23;

Length 411; Indels

Gaps

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299

part of the printed directly from WIPO

03-SEP-2001

(first entry)

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RESULT
AAX89287
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밁
                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the proteins are collectively known as colon cancer antigens. The colc cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer-associated nucleic acid molecules (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                     Human regulatory protein HRGP-3 encoding DNA.
                                                                              21-SEP-1999
                                                                                                                                                             AAX89287 standard; DNA; 1198 BP
                                                                                                                                                                                                                                                                             402 GGCACAATGATAAACATACTGGCTGTTGTTGGTGACAATGACC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention.
                                                                                                                                                                                                                                                         125 ggcacaatgataaacatactggctgttgtggtgacaatgacc 166
                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-235357/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG76406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to AAH37195 and AAG73514 to AAG77788 represent human colon ssociated nucleic acid molecules (N) and proteins (P), wher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 4574-4575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                 94 A; 70 C; 93 G; 78 T;
                                                                                                                                                                                                                                                                                                                                                      3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                    score 42;
s; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding cDNA SEQ ID NO: 2893
                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen
                                                                                                                                                                                                                                                                                                                                                        DB 22;
4.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence listing were sequences are present
                                                                                                                                                                                                                                                                                                                                                                           Length 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present ... (P), where proteins (P), where
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are present
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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Regulatory protein; HRGP; human; cell proliferation; immune response;

Дb ρy

Query Match Best Local Matches

19; Conser

BP;

377

Α;

227

C; 266

G;

328

Τ;

0 other;

Conservative

0;

Mismatches

1.5%;

Score 19; pred. No.

DB 16;

20; 0;

Length 1198;

0;

Gaps

0;

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diabetes mellitus; emphysema; atrophic gastritis; glomerulonaphritis; gout; Grave's disease; hypersinophillia; irritable bowel syndrome; ALD; lupus erythematosus; multiple sclerosis; myasthemia gravis; infarction; osteoarthritis; osteoporosis; pancreatitis; polymyositis; hemodialysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides novel human regulatory proteins (AAY28915-926), designated HRGP, and their polynucleotides (AAX89285-296). The proteins can be produced using standard recombinant technology. The expression of HRGP is closely associated with cell proliferation and the polypeptides and polynucleotides are useful in the diagnosis, treatment and prevention of diseases associated with cell proliferation, particularly immune responses and cancer. The protein or agonists may be administered to treat or prevent a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma mucloma cancer such as adenocarcinoma, leukemia, lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus; Crohn's disease; ulcerative colitis; atopic dermatitis; dermatomyositis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;
tetracarcinoma; Addison's disease; adult respiratory distress syndrome;
allergy; anemia; asthma; atherosclerosis; bronchitis; cholecystitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Au-young J, Bandman O,
Lal P, Shah P, Tang Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis; scleroderma; Sjoegren's syndrome; and autoimmune thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain, cervix, breast, gail bladder, ganglia, ovary and pancreas. Where HRGP is promoting leukocyte activity or proliferation, antagonists which decrease the activity of HRGP are administered. Such responses may be associated with disorders such as Addison's disease, adult respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 82; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; trauma; ss
                                                                                                             osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjoegren's syndrome, and autoimmune thyroiditis, complications of cancer, hemodialysis, extracorporeal circulations
                                                                                                                                                                                                                                   gastritis, gout, glomerulonephritis, Grave's disease, hypersinophillia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthemia gravis, myocardial or pericardial infarction, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                distress syndrome, AIDS, allergies, anemia, asthma, atherosclerosis, bronchitis, cholecystitus, Crohn's disease, ulcerative colitis, atopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human regulatory proteins, useful for diagnosing, preventing and treating disorders associated with expression of regulatory proteins
                           bacterial, fungal, parasitic, protozoan, and helminthic in
trauma. The HRGP polynucleotide may be used for diagnosis
                                                                                                                                                                                                                                                                                                                                                                           dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   but are not limited to, cancers of the adrenal gland, bladder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanoma, myeloma, sarcoma, and tetracarcinoma. Such cancers include,
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0001403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US27471
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source of primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corley NC, Yue H;
                                                                                                                 syndrome, and autoimmune thyroiditis, hemodialysis, extracorporeal circulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guegler KJ,
and probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JL;
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RESULT 23
AAZ52867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a huminate composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human nucleic acid sequences from proteins
                                                           nephrotropic; antiinfective; antibacteria; gene t
neural disorder; immune system disorder; muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY73841,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1999
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                                                                                                                                                                                                                           Human colon cancer antigen nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                 09-MAR-2001
                                                                                                                                                                                                                                                                                                                                  AAC98069;
                                                                                                                                                                                                                                                                                                                                                                                     AAC98069 standard; cDNA; 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1202 BP; 381 A; 227 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids derived from human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel polypeptides and their encoding nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pancreas; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ52867
                                                                                                                         immunomodulatory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (META-) METAGEN
                     infectious disease; cardiovascular disorder; ss
                                                                                                                                            identification; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 tccctcagacttgggaaga 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 TCCCTCAGACTTGGGAAGA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 189-190; 502pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                     cancer; colon cancer antigen;
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DE-1020190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY73842, AAY73843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                           gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1202
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                                                                                         gynaecological; gastrointestinal;
; antibacterial; gene therapy; wou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                               cardioactive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor tissue which have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                          diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                            gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                             NO:79
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                                                                                                                                               vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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peripheral nervous system;

Human; nootropic; immunosuppressant; cytostatic;

amyotrophic lateral sclerosis; Shy-Drager Syndrome;

drug

arthritis;

inflammation;

Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

neuropathy;

central

nervous system;

cancer;

Human polynucleotide SEQ ID NO 3667

22-OCT-2001

(first entry)

WO200153312-A1

Homo sapiens.

chemokinetic; eukaemia; ss

В Ş

Matches Query Match

Conservative

0;

Mismatches

0;

0;

Gaps

100.0%; 1.5%;

Score 19; Pred. No.

16; 21;

Length 1215; Indels

Best Local Similarity

AA159678

25

AAI5967,8 standard; cDNA; 1536

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can be used in gene therapy. The colon cancer antigen polynucleotides proteins and antibodies to the proteins are useful for the prevention treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins
                                                                                                    may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification of the present and the sequences used in the exemplification and the sequences used in the sequences
Sequence 1215 BP; 381 A; 232 C; 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 524; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colon cancer associated gene sequences, antigens, useful for the treatment, pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-') HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary, nephrotropic, antiinfective and antibacterial activities, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The colon cancer antigen polynucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ces, referred to prevention, and
329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            for the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as colon cancer
diagnosis of co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of colon
                                                                                                                present
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Best Local Similarity Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system, such as peripheral nervous injuries, peripheral neuropathy a localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442253/47.
P-PSDB; AAM40522.
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03-AUG-2000,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3667; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1536 BP; 443 A; 365 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.N.S disorders.
Note: The sequence data for this patent did
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                                                     peripheral nervous system; neurop
Alzheimer's; Parkinson's disease;
                                                                                                                                       Human polynucleotide SEQ ID NO 3668
                                                                                                                                                                                  22-OCT-2001 (first entry)
                                                                                                                                                                                                                         AAI59679;
                                                                                                                                                                                                                                                                AAI59679 standard; cDNA; 1536 BP.
Leukaemia;
                   chemokinetic; thrombolytic;
                                                                                                Human; nootropic;
                                                                                                                                                                                                                                                                                                                                                                       346
                                                                                                                                                                                                                                                                                                                                                                                                            58 GTGGCAGCGGCGGCAG 76.
                                                                                                                                                                                                                                                                                                                                                                     gtggcagcggcggcag
                                                                                                                                                                                                                                                                                                                                                                                           HYSEQ INC
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                   Conservative (
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Wehrman T, X
, Goodrich R,
                                                                                                immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                          364
                                                                             neuropathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19;
Pred. No.
                                      Shy-Drager Syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                            Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 T;
                                                                                 ytostatic; gene therapy; central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                            inflammation;
                                                                haemostatic;
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AAV81267
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
"hehes 19; Conserve
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypurcleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang
                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              assays for receptor activity, arthritis and inflammation, leukaemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's. Parkinson's diseases unriversely and diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
P-PSDB; AAM40523.
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                                                                                                                                                                                                                                                                                                               Sequence 1536 BP;
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                                                                                                                             AAV81267 standard; cDNA;
                                                  Bcl-2 interaction
                                                                            11-MAR-1999
                                                                                                      AAV81267
                                                                                                                                                                                          346 gtggcagcggcggcggcag
                                                                                                                                                                                                                       58 GTGGCAGCGGCGGCAG 76
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                                                                                                                                                                                                                                                                                                                                                     disorders. The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYSEQ INC
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3668; 10078pp; English
                                                                                                                                                                                                                                                  Conservative
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2000US-0662191.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                  443 A;
                                                   protein
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                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                  365 C;
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                                                   encoding cDNA
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Xu C, Xue AJ,
R, Drmanac RT;
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Pred. No.
                                                                                                                                                                                                                                                                                                                  399 G;
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                                                                                                                                                                                                                                                                                                                     329 T;
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16;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                           not form
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Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                      Gaps
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Bcl-2 interaction protein; Bis; molecular mechanism; apoptosis; diagnosis; prevention; treatment; ss.

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RESULT 28
AAZ51797
ID AAZ517
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  Query Match
Best Local Similarity
Matches 19; Conserv
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              09-SEP-1998;
                                         09-SEP-1999;
                                                                                                                                                                                                                 Human BAG-3; Bcl-2 associated athanogene-3; apoptosis; cell migration; tumour cell metastasis; Hsc70/Hsp70-regulating protein; metastasis; tumour cell proliferation; steroid hormone receptor function; ss.
                                                                                                                                                                                                                                                                         Full length cDNA sequence for human BAG-3 protein.
                                                                                                                                                                                                                                                                                                     04-JUL-2000
                                                                                                                                                                                                                                                                                                                                AAZ51797;
                                                                                                                                                                                                                                                                                                                                                          AAZ51797 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 12-15; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Bcl-2 interaction protein gene (Bis) - useful for elucidation of the molecular mechanism of apoptosis, and in diagnosis, prevention and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1997;
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                                                                    16-MAR-2000,
                                                                                              WO200014106;A1
                                                                                                                                                                                            Homo
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DB; AAW95196.
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              98US-0150489
                                         99WO-US21053
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                                                                                                                      /*Cag= a
/product= "Human BAG-3 protein"
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%;
                                                                                                                                                                                                                                                                                                                                                          2528 BP
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Pred. No.
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16;
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ID AAZ5
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Best Local s
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      athanogene-3) protein. BAG is a Hsc70/Hsp70-regulating protein (Hsc70/Hsp70 is a molecular chaperone that participates in controlling
                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAG-1 related proteins from humans, Caenorhabditis elegans and Schizosaccharomyces pombe useful for modulating tumor cell proliferation, cell migration and metastasis and steroid hormon receptor function
(BURN-) | BURNHAM INST
                         09-SEP-1998;
                                                    09-SEP-1999;
                                                                               16-MAR-2000.
                                                                                                         WO200014106-A1
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                  tumour cell proliferation;
                                                                                                                                                                                                                                             Human BAG-3; Bcl-2 associated athanogene-3; apoptosis; cell migration; tumour cell metastasis; Hsc70/Hsp70-regulating protein; metastasis;
                                                                                                                                                                                                                                                                                       Full length expanded cDNA sequence
                                                                                                                                                                                                                                                                                                                  04-JUL-2000
                                                                                                                                                                                                                                                                                                                                           AAZ51804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2528 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein bioactivity, degradation, complex assembly/disassembly and translocation across membranes). It competes with Hip for binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present cDNA sequence encodes human BAG-3 (Bcl-2 associated athanogene-3) protein. BAG is a Hsc70/Hsp70-regulating protein
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DB; AAY70508.
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19; Conservative
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                         9805-0150489
                                                      99WO-US21053
                                                                                                                                 /product=
                                                                                                                                                              Location/Qualifiers 307..2034
                                                                                                                                                    /*tag=
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                                                                                                                                   "Human BAG-3 protein"
                                                                                                                                                                                                                                   steroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 G;
                                                                                                                                                                                                                                                                                       for human BAG-3 protein.
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17;
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                                                                                                                                                                                                                                   receptor function; ss
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2000-256937/22 AAY70515

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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cellular phenotypes through their interactions with Hsc70/Hsp70,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     including increasing resistance to apoptosis, promoting cell proliferation, enhancing tumour cell migration and metastasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translocation across membranes). It competes with hip for binding to the Hsc70/Hsp70 ATPase binding domain and promotes substrate release. Gene transfection studies indicate that BAG proteins influence a wide variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      athanogene-3) protein. BAG is a HSC/U/HSp/U-regulating protein (HSC70/HSp70 is a molecular chaperone that participates in controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present expanded cDNA sequence encodes human BAG-3 (Bcl-2 associated athanogene-3) protein. BAG is a Hsc70/Hsp70-regulating protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe useful for modulating tumor cell proliferation, cell migration and metastasis and steroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2534 BP; 596 A; 806 C;
WPI; 1999-059908/05.
P-PSDB; AAW88287.
                                                                                                                                                                                                                                                                                                                                                         Rattus rattus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV84294 standard; DNA; 3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP/ATP exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein bioactivity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor function
                                                                                                                                                                                                                 04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              Selectable marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat (Na,K)-ATPase alpha 1 subunit (L879C mutant) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV84294
                                                                          Belusa R;
                                                                                                                                                                     04-JUN-1997;
                                                                                                                                                                                                                                                              10-DEC-1998
                                                                                                                                                                                                                                                                                                               WO9855603-A1
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                                                                                                                      KAROLINSKA INNOVATIONS AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                     97SE-0002120.
                                                                                                                                                                                                                    98WO-SE01062
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Na,K)-ATPase; rat; gene therapy; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degradation; complex assembly/disassembly and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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New mutated (Na,K)-ATPase

useful as a selection marker

mutation, obtained by mutagenesis of the (Na,K)-ATPase gene (see AAV84297), causes a loss in sensitivity of the encoded enzyme to ouabain. A claimed method for detecting transfection or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO
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RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transfecting the cell with a vector carrying a nucleic acid encoding a mutated (Na,K). ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibrinogen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new selectable marker is particularly useful where antibiotic resistance selection is undesirable, e.g. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ouabain. A claimed method for detecting transfection or transformation of a eukaryotic cell comprises: (a) transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat protein (see AAW88290) has been mutated to cysteine. This mutated protein can be used as a novel selectable marker. The mutation, obtained by mutagenesis of the (Na,K)-ATPase gene (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This nucleotide sequence encodes a new mutated 1 subunit (see AAW88287), in which the Leu-879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 45-49; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV84295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3636 BP; 850 A; 967 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV84297),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selectable marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV84295
                                           This nucleotide sequence encodes a new mutated (Na,K)-ATPase alpha 1 subunit (see AAW88288), in which the Leu-881 residue of the native rat protein (see AAW88290) has been mutated to cysteine. This mutated protein can be used as a novel selectable marker. The
                                                                                                                                                                                                   WPI; 1999-059908/05
P-PSDB; AAW88288.
                                                                                                                                                                                                                                                                                                                   04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                   04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                WO9855603-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat (Na,K)-ATPase alpha 1 subunit (L881C mutant) DNA
                                                                                                                                 Disclosure; Page 49-53; 72pp; English.
                                                                                                                                                                New mutated (Na,K)-ATPase - useful as a selection marker
                                                                                                                                                                                                                                                    Belusa R;
                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1998;
                                                                                                                                                                                                                                                                                  (KARO-) KAROLINSKA INNOVATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GTGGCAGCGGCGGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 gtggcagcggcggcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 100
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 3636 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     causes a loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                   97SE-0002120
                                                                                                                                                                                                                                                                                                                                                   98WO-SE01062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Na,K)-ATPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in sensitivity of the encoded enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         995 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          824 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 3
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transformation of a eukaryotic cell comprises: (a) transforming or transfecting the cell with a vector carrying a nucleic acid encoding a mutated (Na,K)-ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibrinogen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new selectable marker is particularly useful where antibiotic resistance selection is undesirable, e.g. in gene therapy.
                                 interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibrinogen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new
                                                                                                          This mutated protein can be used as a novel selectable marker. The mutation, obtained by mutagenesis of the (Na.K)-ATPase gene (see AAV84.297), causes a loss in sensitivity of the encoded enzyme to ouabain. A claimed method for detecting transfection or transformation of a eukaryotic cell comprises: (a) transforming or transfecting the cell with a vector carrying a nucleic acid encoding a mutated (Na.K)-ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardioglycoside such interest; (b) incubating the cells with a cardioglycoside such
                                                                                                                                                                                                                                                                                                                                                This nucleotide sequence encodes a new mutated 1 subunit (see AAW88288), in which the Leu-879
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 54-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV84296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-059908/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Belusa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-1999
               selectable marker is particularly useful where antibiotic resistance
                                                                                                                                                                                                                                                                                                                         the native rat protein (see AAW88290) have been mutated to cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW88289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KARO-) KAROLINSKA INNOVATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GTGGCAGCGGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 gtggcagcggcggcag 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Na,K)-ATPase - useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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undesirable,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Na,K)-ATPase;
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                                                                                                                                                                                                                                                                                                                                                                                                                            72pp; English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selection marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Τ;
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                                                                                                                                                                                                                                                                                                                                                (Na,K)-ATPase alpha and Leu-881 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3636;
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Best Local Sin
Matches 19;
                                          Matches
                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3636 BP;
                                                                                                                                                                 as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibrinogen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new
                                                                                                                                                                                                                     enzyme to ouabain. A claimed method for detecting transfection or transformation of a eukaryotic cell comprises: (a) transforming or transfecting the cell with a vector carrying a nucleic acid encoding a mutated (Na,K)-ATPase gene of the invention, plus a gene
                                                                                                                                                                                                                                                                                                                          This nucleotide sequence enc
subunit (see AAW88290). (Na
essential to the cell. The
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                                                                                                                                                                                             of interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouaba
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 59-63; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW88290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belusa R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat (Na,K)-ATPase alpha 1 subunit gene coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-1999
                                                                                                           Sequence
                                                                                                                                                       selectable markers are
                                                                                                                                                                                                                                                                                 gene (see
                                                                                                                                                                                                                                                                                          essential to the cell. The invention provides new, mutated (Na,K)-ATPases (see AAW88287-89) that can be used as novel selectable markers. Appropriate mutation of the (Na,K)-ATPase
                                                                                                                                                                                                                                                                                                                                                                                                           New muťated (Na,K)-ATPase - useful as a selection marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KARO-) KAROLINSKA INNOVATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1998
                                                                                                                                       resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GTGGCAGCGGCGGCGGCAG
58 GTGGCAGCGGCGGCAG 76
                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
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S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-059908/05
                                          19;
                                        Similarity 100
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                           3636 BP; 850 A;
                                                                                                                                                                                                                                                                                 AAV84294-96)
                                                                                                                                        selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97SE-0002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-SE01062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     850 A; 966 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Na,K)-ATPase;
                                                                                                                                                                                                                                                                    96) causes a loss in sensitivity of the encog
A claimed method for detecting transfection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                     1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%;
                                                                                                                                                     particularly useful where antibiotic
                                                                                                                                       undesirable,
                                                                                                             968 C;
                                                                                                                                                                                                                                                                                                                                        encodes the rat (Na,K)-ATPase alpha
(Na,K)-ATPase is an ion transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                        0;
                                                     Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
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                                                                                                             995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 G;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rat;
                                                                                                             <u>ი</u>
                                                                                                                                     e.g.
                                                                                                                                                                                                                                                                                 in sensitivity of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 T; 0 other;
                                                                                                             823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                        DB
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
17;
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                                                                                                             T; 0
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                                                                    20;
                                                                                                                                        gene
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                                        0;
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                                                                 Length 3636;
                                                                                                             other,
                                                                                                                                        therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                          Indels
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                                        0;
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                                        Gaps
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В

28

gtggcagcggcggcag

46

AAF44683 RESULT

34

AAF44683 standard;

CDNA; 7328

BP

27-MAR-2001 AAF44683;

(first entry)

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Дb
                                                γQ
                                                                                                         Query Match
Best Local Similarity
Matches 19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; protein kinase; antiarthritic;
immunosuppressive; cardiant; renal; antiinfl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protein
                                                                                                                                                                                                                                                                                                                        expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction. immune disorders, cardiomyopathies, strokes, renal fallure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes' a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease neurodegenerative diseases and/or cancers \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory pelvic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementary sequences may also be used as DNA probes in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 2; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-032161/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000WO-US14842.
                                                                                                                                                                                                                                                            Sequence 7328 BP; 2036 A; 1850 C; 1655
                                                                                                                                                                                                                                                                                                                     reproductive disorders.
58 GTGGCAGCGGCGGCAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinez
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0136503
                                                                                                                                                1.5%; Score 19;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple sclerosis;
                                                                                                                           0;
                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sudersanam
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                                                                                                                                                                                                                                                                     G; 1785 T;
                                                                                                                                                      DB
17;
                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisclerotic; osteopathic;
                                                                                                                              0;
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                                                                                                                                                                                    Length 7328
                                                                                                                                                                                                                                                                           2 other;
                                                                                                                              Indels
                                                                                                                                 0;
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AAZ38983

XEXEX

(first entry)

EST clone D1482 15-FEB-1999 AAV90298 В . Qy

Query Match
Best Local Similarity
Matches 18; Conserv

Conservative

0;

Mismatches

0

Indels

0,

Gaps

0,

100.0%;

Score 18; Pred. No.

DB 21; Length 30;

872 ATTGTGGATGCTTTACCA 889 

AAV90298 RESULT

AAV90298 standard; cDNA; 346

ВP

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XX
YQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YXX PD XXX
    1,3-propanediol; vitamin Bl2 transport; glycerol dehydratase; BtuB; 1,3-propanediol oxidoreductase; vitamin Bl2 receptor precursor; BtuC; vitamin Bl2 transport system permease protein; BtuD; polyester fibre; vitamin Bl2 transport ATP-binding protein; polyurethane; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ38983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ38983 standard; DNA; 30
                                                                                                                                                         The present invention describes the monomer, 1,3-propanediol (I), which is biologically produced by using a transformed host cell (C) comprising at least one copy of gene encoding BtuB, BtuC and BtuD. (I) is produced by the steps comprising: (1) contacting the transformed (C) with at least one fermentable common source and an effective amount of vitamin B12. The transformed (C) comprises at least one copy of genes encoding a protein having dehydratase activity (a), a protein having an oxidoreductase activity (b), a vitamin B12 receptor precursor protein (C), a vitamin B12 transport system permease protein (d), and a vitamin B12 transport system permease protein (d), and a vitamin B12 transport by the permease protein (d), and a vitamin B12 transport by the permease protein (d).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whited GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1999;
                                      ATP or GTP-binding protein (e); and (2) recovering (1) produced by (1). The method is used to produce (1) which is employed in the manufacture of polyester fibre, polyurethane and cyclic compounds. The method produces 1,3-propanediol rapidly and it is inexpensive. The present sequence represents a primer used in the construction of expression vectors in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           Production of a monomer which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-053104/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1998;
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Sequence 30 BP; 8 A; 4 C; 6 G;
                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 56; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        fiber, polyurethane and cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector construction primer SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                              compounds
            12 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gatenby AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    the manufacture of polyester
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins e.g. human blood, kidney, foetal lung, placenta, test ovary, pituitary, retina and colon cDNA libraries.
                                                                                                 Human; 5' Esi,
gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-070077/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1997;
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21-FEB-2000; 2000EP-0200610.
                          06-SEP-2000
                                                     EP1033401-A2
                                                                                                                                                                      06-OCT-2000
                                                                                                                                                                                                                          AAC01530 standard; cDNA; 402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemotactic/chemokinetic activity, haemostatic and thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 496; 618pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                 266
                                                                                                                                                                                                                                                                                                                         680 GGAAAACCAGAAAATGAG 697
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                        37
                                                                                                                                                                                                                                                                                              ggaaaaccagaaaatgag
                                                                                                                                                                                                                                                                                                              5' EST;
                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o MJ, vac.
A, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue growth activity, activin/inhibin activity,
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                      (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
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paulding V,
                                                                                                        chromosome
                                                                                                                                              protein 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                                                                                               1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                        A; 62 C; 101
                                                                                                     sequence tag; secreted protein; cDNA isolation; mapping; ss.
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Treacy M;
                                                                                                                                              EST,
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                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   DB
51;
                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 other;
                                                                                                                                              1528
                                                                                                                                                                                                                                                                                                                                                                               20; Length 346;
                                                                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                                                                       Indels
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AAF11454/c
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Best Local Similarity
Matches 18; Conserv
                                                                          (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNAs and even in those cases, where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                  22-MAR-1999;
                                                                                                                                                                                                                                                                                                  22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200056762-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger EST SEQ ID NO:3977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF11454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF11454 standard; cDNA; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from 30 different tissues. EST sequences usually correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 1528; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 GGAAAACCAGAAAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 ggaaaaccagaaaatgag 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resent sequence is one of a large number of 5' ESTs derived from encoding secreted proteins. An ORF has been identified within the nce. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                          NOVO NORDISK BIOTECH INC. NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                  99US-0273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 Ą;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        engineering; catabolic pathway engineering; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    рв
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Berka RM,

Rey MW,

Shuster JR,

Kauppinen

s

Clausen

IG,

Olsen PB

2000-594572/56

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RESULT 39
AAH13135/c
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                                                                                                                                                                                                                            XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of genes in uses fluorescence-labeled nucleic acids isolate substrate of expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of genes in a first filamentous expression of the same genes in one or mor cells. The method uses fluorescence-labele the FF cells and a substrate of expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on array equals one gene or open reading frame, and organisation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   same genes in one or more second filamentous fungal cells. Monitor the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention
                                      29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monitored.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a first
                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone (3'-primer) SEQ ID NO:9970
(HELI-) HELIX RES
                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH13135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH13135 standard;
                                                                                                                                                                 28-JUL-2000;
                                                                                                                                                                                                        07-FEB-2001.
                                                                                                                                                                                                                                             EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GGCAGCGGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GGCAGCGGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1764; 3161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The expression of genes can be used to study how FF cells
                                         99JP-0248036
99JP-0300253
2000JP-0118776
2000JP-0183767
2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                 2000EP-0116126
                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 A; 128 C; 121 G; 166 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              same genes in one or more second filamentous fun uses fluorescence-labeled nucleic acids isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 18;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       describes a method for monitoring differential n a first filamentous fungal (FF) cell relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enes in filamentous fungal cells isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags (EST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FF) cell relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        filamentous fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells. Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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PI PI
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Ishii S,
                                                                                                                                                                                                                               primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                     The present full-length
                                                                                                                                                                                                               Claim 3; SEQ ID 9970;
                                                                                                                                                                                                                                                                                           Isogai T,
, Sugiyama
                                                                                                                                                                                                invention describes primer sets
                                                                                                                                                                                                                                                                                            Nishikawa
T, Wakama
                                                                                                                                                                                                                 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                             Wakamatsu
                                                                                                                                                                                                                                                                                                     Τ,
                                                                                                                                                                                                                                                                                              Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                              Saito K, Yamamoto, Otsuki T;
                                                                                                                                                                                                 synthesising
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and to the complementary service of an oligonucleotide sequences defined in the specification, where oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the of an oligonucleotide comprises a sequence comprises a 5'-end particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 without are specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB92446 to AAH36393 represent oligonuclectides, all of which are used in the exemplification represent oligonuclectides, all of which are used in the exemplification to the complementary strand of a polynucleotide which comprises one the 5602 nucleotide sequences defined in the specification. full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary complementary strand of a polynucleotide which comprises a in gene therapy. The particularly full-The primers are useful for synthesising polynucleot 1-length cDNAs. The primers are also useful for the a combination eotides of

Sequence 582 BP; 142 A; 120 Ç 83 G; 229 T; 8 other;

Qγ Ouery Match Best Local Similarity Matches 18; Conserv 870 CCATTGTGGATGCTTTAC Conservative 1.4%; 887 0; Score 18; Pred. No. Mismatches DB 51; 22; .0; Length 582; Indels 0; Gaps

0;

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RESULT
                                                밁
AAH67523/c
ID AAH67523 standard; DNA; 588
                                                106
                   40
                                                CCATTGTGGATGCTTTAC
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AAH67523

26-SEP-2001 (first entry)

C glutamicum coding sequence fragment SEQ ID NO: 2558 organic Coryneform acid bacterium; amino id synthesis; ds. acid synthesis; vitamin; saccharide;

Corynebacterium glutamicum

EP1108790-A2

18-DEC-2000; 2000EP-0127688

20-JUN-2001

16-DEC-1999; 07-APR-2000; 03-AUG-2000; 99JP-0377484. 2000JP-0159162. 2000JP-0280988.

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RESULT 41
AAF11560/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                          (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                particularly L-lysine. The present sequence is a nucl in the exemplification of the invention.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant of coryneform bacterium, measuring expression amount an analysing the expression profile or expression pattern of a ge from Coryneform bacterium, and identifying a homologue of a gram coryneform bacterium. Coryneform bacteria are useful for amino acids, nucleic acids, vitamins, saccharides and organic particularly L-lysine. The present sequence is a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are useful for identifying the mutation point of a gene derived from mutant of coryneform harterium massuring for the massuring for the massuring for the massuring for the first form the form that the form the 
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Tateishi
WPI; 2000-594572/56
                                                                                                                                                                  22-MAR-1999;
                                                                                                                                                                                                            22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                   Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF11560 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus niger
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                                                                                          NOVO
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                                              Rey MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                          NORDISK BIOTECH INC NORDISK AS.
                                                                                                                                                                                                              2000WO-US07781.
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Senoh A, Ikeda
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                                              Shuster
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da M, Ozaki A;
                                              JR,
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Pred. No.
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                                            Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Listing; English
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51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                         Clausen IG,
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                                         Olsen
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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
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Claim 87; Page 1796; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microorarrays based on function of the gene products to facilitate enaltysis of the results. AAF07478 to AAF11847 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF11854 to AAF11857 from Trichoderma reesei, which are all specifically claimed in the present invention.

Sequence 593 BP; 104 A; 198 C; 160 G; 124 T; 7 other;

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Query Match 1.4%; Score 18; DB 21; Length 593;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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В 6

59 TGGCAGCGGCGGCAG

76

286

TGGCAGCGGCGGCAG

RESULT 42
AAT37915/c
ID AAT37915,standard; cDNA; 624 BP.
XX
AC AAT37915;
XX
DT 28-APR-1997 (first entry)
XX
VEGF-B186 coding sequence.

Endothelial cell; proliferation; vascular endothelial growth factor; VPF; VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration; vascular permeability factor; cell mitogen; angiogenesis; cell growth; embryonic development; wound healing; tissue reorganisation; antibody; cancer; metastatic risk; tumour cell; mouse; ss.

Homo sapiens.

WO9626736-A1.

06-SEP-1996.

01-MAR-1995; 95US-0569063.

01-MAR-1995; 95US-0397651.

06-JUN-1995; 95US-0469427.

(LUDW-) LUDWIG

INST CANCER RES

PT PT CCC

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RESULT 43
AAV63569/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alitalo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT37909-T37915 represent the coding sequences for the vascular endothelial growth factor (VEGF) proteins of the invention, which profession the invention of the invention, which professions the invention of the invention of the vascular endothelial or mesodermal cell proliferation. VEGF is also a endothelial or mesodermal cell proliferation. VEGF is also a gradual proliferation of the vascular glycosylated cationic dimer, and is sometimes referred to as vascular glycosylated cationic dimer, and is sometimes referred to as vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 61-62; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          permeability factor (VPF). VEGF has diverse effects, depending on t specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenessis in vivo by promoting endothelial cell growth during nor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonic development, wound healing, and tissue regeneration/reorganisation. The VEGF proteins of the invention share regeneration/reorganisation. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and the angiogenic and other properties of VEGF. The proteins can therefore be expressed in tissues differently to VEGF. The proteins can therefore be expressed in tissues differently to VEGF. The proteins the used to accelerate angiogenesis in wound healing. Antibodies can proteins can be used for inhibiting angiogenesis. The antibodies can proteins can be used diagnostically to quantitatively detect VEGF. In primers also be used diagnostically to quantitatively detect VEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementary to the coding sequences for the proteins of the invention can also be used to detect VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy specimens may be useful as an indicator of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF coding sequences, this is antisense sequences direct against the VEGF coding sequences, this is especially useful in retarding VEGF expression in tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV63569 standard; cDNA; 624 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV63569;
                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor; VEGF; proliferation; human; endothelial cell; angiogenesis; tissue growth; organ repair; ss
                                                                                                                                                                                                                                                                                                                                                               cDNA clone
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                                                                                                                                                                         CDS
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01-MAR-1996;
                                         24-NOV-1998
                                                                                   US5840693-A.
                                                                                                                                                                                                                                            Homo sapiens
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DB; AAW04831
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                                                                                                                                                                                                                                                                                                                                                             encoding vascular endothelial growth factor (VEGF)-B186
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    96US-0609443
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                  /product= VEGF-B186
                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u,
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pred. No.
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51;
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also related
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RESULT 44
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01-MAR-1995;
06-JUN-1995;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VEGF)-B186. VEGF proteins are used for promoting proliferation of endothelial cells and for stimulating angiogenesis (the proliferation of new capillaries form pre-existing blood vessels). These activities of new capillaries form pre-existing blood vessels). These activities are useful for treating tissue growth and repair, including organ repair. This is also useful in pregnancy, in follicle development, as these processes must occur in development of the placenta. The as these proteins can also be used to raise antibodies, either for use in detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action. This is detection of the proteins or as inhibitors of their action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor-B iso:forms, and DNA encoding them - useful for inducing angiogenesis and cellular proliferation, and raising antibodies to inhibit activities in e.g. tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-034079/03.
P-PSDB; AAW80495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes human vascular endothelial growth factor (VEGF)-B186. VEGF proteins are used for promoting proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 624 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA91005 standard; DNA;
                                                                                                                                                                                                                                                                                                                    Human; angiogenic protein; wound healing; vascular tissue repair; peripheral arterial disease; critical limb ischaemia; coronary di
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA91005;
                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                              Human VEGF-3 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2001
                                                                                                                                                                                                                                                                                                    angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              585
                                                                                                                                                       Key
                                                                                                                                                                                                                                                  vascular endothelial growth factor-3;
               01-JUN-2000; 2000WO-US14925
                                                                                                                                                                                                                                                                                   rheumatoid
                                                                                                                                                                                                                                                                     infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                  14-DEC-2000
                                                                                   WO200075163-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAGCGGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAGCGGCGGCAGG 77
                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 14; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eriksson U,
                                                                                                                                                                                                                                                                     arthritis; autoimmune disease; disease; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0397651.
95US-0397651.
95US-0469427.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                      tumour; inflammation; diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 A; 235 C; 179 G; 104 T; 0 other;
                                                                                                                                                                            Location/Qualifiers
                                                                                                                            /product= VEGF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB
Pred. No. 51;
0; Mismatches
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                                                                                                                                                                                                                                                                 VEGF-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
51;
                                                                                                                                                                                                                                                                                                  allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                    retinopathy; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                   SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                         coronary disease;
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03-JUN-1999;

99US-0137796

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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The antibodies are useful as therapeutic (ant)agonists; for detection, purification and targeting of proteins for in vivo or in vitro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytotoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoting head
critical limb
                                                                                                                                                                                          Plant; lignin;
Pinus radiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    range of other disorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases (viral, bacterial, fungal or parasitic); neurodegeneration, also as chemotactic agents or for stimulating regeneration of the nervous system etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increased vascular permeability), diabetic retinopathy, rheumato arthritis or psoriasis. Agonists are also useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat inflammation (where associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detecting mutations or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, and for repair of vascular tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 224; 244pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease. critical limb ischaemia or coronary disease
                                                                                                    WO200022099-A1
                                                                                                                                                Pinus radiata
                                                                                                                                                                                                                                              Pinus radiata flavonol glucosyl transferase DNA sequence SEQ ID NO:218
                                                                                                                                                                                                                                                                                                   24 -OCT - 2000
                                                                                                                                                                                                                                                                                                                                            AAA68125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 624 BP; 106 A; 235 C; 179 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (lymph)angiogenesis. The proteins are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially peripheral arterial disease, critical limb ischaemia
                   06-OCT-1999;
                                                               20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                    AAA68125 standard; DNA; 762 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ameliorate disease and to detect diseases, or susceptibility, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 GGCAGCGGCGGCGGCAGG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GGCAGCGGCGGCAGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch is an angiogenic protein of the invention. The angiogenic proteins the DNA sequences encoding them, are used to prevent, treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                          Monterey pine; ds
                                                                                                                                                                                                         lignin biosynthetic pathway; Eucalyptus grandis;
                   99WO-NZ00168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hu J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tactor-3 (VEGF-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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which are involved in the lighin biosynthetic pathway. The polynucleotides can be used for modulating lighin content, lighin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighin biosynthetic pathway, and for producing a plant having altered lighin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The lighin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                  laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, caffetc acid methyl transferase, caffeoyl CoA methyl transferase, comerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavano glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                             coniferol glucosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                      coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase
(OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 124; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-317962/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloksberg LN, Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD (FLET-) FLETCHER CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention, describes isolated polynucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                                 phenylalanine ammonia-lyase (PAL),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    representing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0169789
99US-0143811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the enzymes cinnamate 4-hydroxylase
                                                                                                                                                                                                                                                                                                                                                                             (CGT), coniferin beta-glucosidase (CBG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTD.
                                                                                                                                                                                                                                                                                                                                                                                               4-coumarate:CoA ligase (4CL)
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(C4H)

Sequence 762 BP; 227 A; 131 C; 202 G; 202 T; 0 other

Query Match, Best Local Similarity Matches 18; Conser 764 CATTGGAAAGCATTAGTG 781 Conservative 100.08; Score 18; Pred. No. Mismatches DB 21; 51; Length 762; 0; Gaps 0

Search completed: March 29, 2002, 20:56:33 Job time: 2153 sec

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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-328-11-577

US-09-154-083-31

US-09-097-072-1

US-08-086-638-1

US-09-097-072-3

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US-08-975-166-5
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PCT-US93-05651-4
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US-09-080-285-19
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US-08-569-063C-14
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                            PCT-US91-00899-13
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3178.770 Million cell updates/sec
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Query Match
Best Local Similarity
Matches 1275; Conserv
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•	US-08-525-058A-7	US-08-393-246-7	US-07-914-281-7	US08-753-038-1	US-08-972-719-1	PCT-US94-00324-2	US-08-428-414A-4	US-08-282-845-1	US-08-006-676B-2	US-08-482-073-10	US-08-482-073-9	PCT-US96-06427-3	US-08-483-151-3	US-08-880-342-16	US-08-365-486A-16	US-09-042-531-9	US-08-696-731-9	US-08-525-058A-9	
	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	<ul> <li>Sequence 4, Appli</li> </ul>	Sequence 1, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 9, Appli	Sequence 3, Appli	· Sequence 3, Appli	Sequence 16, Appl	Sequence 16, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	

## ALIGNMENTS

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CLONE: Consensus
US-08-741-437-2
                                                                                                                                                     TELEFAX: (415) 845:4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                         TUPOLOGY: linear MOLECULE TYPE: cDN
                                                                                                                                                                                                                                                                                                                                                                         CURRENT, APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Filed Her
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER; 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICANT: Hillman, Jennifer L.
TITLE OF INCENTION: A NOVEL HUMAN PYROPHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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STREET: 3174 Por:
CITY: Palo Alto
STATE: California
                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
                                                                                                                                      1275 base pairs
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                                                                                                         CLONE: (US-09-134-593-2
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US-09-134-593.-2
                                             Query Match
Best Local Similarity
Matches 1275; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEFAX: (415) 845-41
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                  LIBRARY:
                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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A NOVEL HUMAN PYROPHOSPHATASE
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 Matches
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[NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
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                                                                                        ORIGINAL SOURCE:
TISSUE TYPE:
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                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-MAR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                NAME: EVANS, JOSEPH REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
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STATE: DC
                                                                                                                                    TOPOLOGY:
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                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER
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Similarity
18; Conserv
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ALITALO, Kari
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Pred. No.
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   Mismatches
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                 DB 2;
12;
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US-08-569-063C-14/c

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INFORMATION:

PPLICANT:

OLOFSSON, ERIKSSON, Ulf

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                                               SEQUENCES
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Patent No. 5459251
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                             TITLE OF INVENTION:
                                  NUMBER OF SEQUENCES: 4
                                                                               APPLICANT: Tsujimoto, Yoshide; Croce, Carlo A.
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
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LENGTH: 624 base pairs
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URRENT APPLICATION DATA:
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APPLICATION NUMBER:
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REGISTRATION NUMBER: :
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                                                                                                                                                                                                                                                                                                                                                                                                                              624 base pairs
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US/08/228,704
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Pred. No.
                                                                                                                                                                                                                                        Mismatches
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12;
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Query Match

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US-08-465-485A-19/c
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08465485A Patent No. 5831066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                       TELEFAX: (408) 436-207 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
                                                                                                                                                                                           PRIOR APPLICATION NUMPER 1992

APPLICATION NUMPER FILING TOTAL NUMPER 1992
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 29
                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 663,010 FILING DATE: 19-MAR-1991 APPLICATION NUMBER: 883,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-APR-1994
                             TYPE:
                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05
CLASSIFICATION:
             STRANDEDNESS:
                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22202
                     nucleic acid
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Y: U.S.A.
                                                                                                                                                                 Fortney,
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linear
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                                                                                                       (408) 436-2070
                                                                                                                                                                                                                                                                                                                                               05-JUN-1995
                                                                                      436-2075
                                                                                                                                                              Andrew D
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100.0%; Pr
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                                                                                                                                                34,600
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Pred. No.
                                                                                                                                     3335-070-55 CONT
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US-09-080-285-19/c
; Sequence 19, Application US/09080285
; Patent No. 6040181
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US-08-365-486A-14/c
                                                                         RESULT
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                                                                                                                                                                            Matches
                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 324-09
WIFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
   APPLICANT: Reed, John
                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                  694 TGGCAGCGGCGGCGGCAG 677
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                                                                                                                                                                                                                                                                                                                                                                  OLECULE TYPE:
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                                                                                                                                               59 TGGCAGCGGCGGCGGCAG 76
                                                                                                                                                                            Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sholtz, Charles K REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                  INFORMATION:
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                                                                                                                                                                         1.4%; Silarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                     linear
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23-DEC-1994
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Pred. No.
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                                                                                                                                                                                         Sequence 14, Application US/08880342 Patent No. 6218179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pair
                                       CORRESPONDENCE ADDRESS
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
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                                                                       TITLE OF INVENTION:
                                                                                                                                  APPLICANT:
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                                                        NUMBER OF SEQUENCES:
                                                                                                    APPLICANT:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          59 TGGCAGCGGCGGCGGCAG 76
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TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: 'Virginia
 CITY:
                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fortney, Andrew REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                            INFORMATION:
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SEE: Dehlinger & Associates
: 350 Cambridge Avenue, Sui
Palo Alto
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                                                                                  Green, Christopher J.
VENTION: Tissue Specific Hypoxia Regulated
                                                                                                                                            Bishopric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (408)
                                                                                                                              Murphy, Brian
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                  Laderoute, Keith R.
                                                                                                                                                          Webster, Keith A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (408) 436-2070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-1992
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22-DEC-1988
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                                                           Therapeutic Constructs
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Pred. No.
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               Suite
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                                                                                                                                                                                                                                                                                                                                                      DB 3;
13;
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Length 5086; Indels

0

Gaps

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

COUNTRY: U: ZIP: 94306

USA

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US-08-880-342-14
PCT-US93-05651-4
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Best Local S
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                                                           FEATURE:
                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                       MOLECULE TYPE:
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PRIOR APPLICATION DATA:
PCT/IB95/00996
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                                                                                                                                                                                                                                                           TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 82
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                               694 TGGCAGCGGCGGCAG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTI-SENSE:
       NAME/KEY: CDS
LOCATION: 1459..2178
OTHER_INFORMATION: /product= "Bcl-2"
                                                                                                                                                                                                                                                                                                                                                                                            59 TGGCAGCGGCGGCGGCAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 23-JU
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sholtz, Charles
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 13-NOV
                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                          TOPOLOGY:
                                                                                                                                                                                                               MEDIUM TYPE: diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
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                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity.
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                                                                                                                   nucleic acid
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                                                                                                                                   5086 base pairs
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                                                                          cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1997
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                                                                                                                                                                                 PCT/US93/05651
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                                                                                                                            RESULT 12 .
5506344-1/c .
Patent No. 5506344
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Best Local Similarity
Watches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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PCT-US93-06251-2/c
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MOLECULE TYPE:
PCT-US93-06251-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: DIGIGLIO, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/-
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 228,704
                                                             NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
                                                                                             APPLICANT: TSUJIMOTO, YOSHIHIDE; CROCE, TITLE OF INVENTION: ANTIBODIES SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 TEGCAGCGGCGGCGCAG 677
                                                                                                                                                                                                                  694 TGGCAGCGGCGGCGCAG 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19930
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                                                                                                                                                                                                                                                                                                                                                                                                                                            5086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516-742-4366
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31,346
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                                              US/08/435,193
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Pred. No.
                                                                                               SPECIFIC FOR BCL-2GENE PRODUCT
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                                                                                                                  CARLO A.
                                                                                                                                                                                                                                                                                                                DB 5;
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13;
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APPLICATION FILING DATE:

NUMBER: 18-APR-1994

994,941

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5506344-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                           FORMATION FOR SEQ
            SEQUENCE CHARACTERISTICS:
                                                     NAME: Kryshak Thad
REGISTRATION NUMBER: 66
REFERENCE/DOCKET NUMBER: 66
FELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                  APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-EEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         SOFTWARE: MSWORD Version 5.0 URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
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                                                                                                                            TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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LENGTH:
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Barney, Michael
Bower, Patricia
                                         (414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cronan, Charles L.
FENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
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19-SEP-1989
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                                       277-5591
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                                                                                    66-005-9234-1
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Pred. No.
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. 13;
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Best Local Similarity
Matches 17; Conserv
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                                       TELEFAX: (414) 277-5591
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                               REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Kryshak, Thad
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 53202
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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มก. 592887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milwaukee
          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08975166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodes, 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tripp, ...
Tripp, ...
Trisk, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cronan, Charles L.
PENTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                    MSWORD Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bower, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barney, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicoye, Etzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thad Kryshak,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide
YES
                                                                                                                                                                                                             28-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 17;
100.0%; Pred. No.
                                                                                                                                                                                                                                                     us/07/917,216
                                                                                                                                                                                                                         US 07/486,333
                                                                                                                                                                                                                                                                                 US/08/180,524
                                                                                                                                                                                                                                                                                                                                         US/08/975,166
                                                                                                                         35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                             66-005-9234-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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OLECULE TYPE:

Oligonucleotide

POPOLOGY:

; HYPOTHETICAL: YES US-08-975-166-5

Matches

58 GTGGCAGCGGCGGCGC 74

Query Match
Best Local Similarity

1.3%; ilarity 100.0%; Conservative (

Score 17; Pred. No.

Length 146; Indels

Mismatches 35 35

0;

Gaps

0;

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US-08-180-524-3
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                  TELEFAX: (414) 277-5591 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No.
                          MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                         REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             FILING DATE: 19-SEF-1907
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
NAME: 35,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 GTGGCAGCGGCGGCGGC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GTGGCAGCGGCGGCGC 74
                                                                     STRANDEDNESS:
                                                          TOPOLOGY:
                                                                                   TYPE: ' nucleic acid
                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: MSWORD Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08180524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodes, ...
Rhodes, ...
                                                                                                    146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cronan, Charles L. / PARTION: METHOD OF EXPRESING ANTIFREEZE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicoye, Etzer
Barney, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bower, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lusk, Lance
                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thad Kryshak, Quarles & Brady
                                                                                                                                                                (414)
                             YES
                                          Other Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edward
                                                                     double
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                                                                                                                                                              277-5707
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                                                                                                                                                                                                                                                                                                                                                                                                        US/08/180,524
                                                                                                                                                                                                                                                                                                                                            US/07/917,216
                                                                                                                                                                                                       35,433
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                                                                                                                                                                                            66-005-9234-1
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34;
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В
; ANTI-SENSE:
US-08-975-166-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08975166
                                                                                                                                          TELEFAX: (414) 277-559
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                           MOLECULE TYPE: OF
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (414) 277-5707
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            FILING DATE: 28-FEB-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                             NAME: Kryshak, Thad REGISTRATION NUMBER:
                                                                             STRANDEDNESS:
                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/917,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Milwaukee
                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wisconsin
                                                                                                          146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicoye, Etzer
Barney, Michael
Bower, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                             (414) 277-5591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodes, Thou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tripp, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lusk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSWORD Version 5.0
                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thad Kryshak, Quarles & Brady
                                                                                                                                                                                                                                                                                JMBER: US 07/409,217
19-SEP-1989
                                              Other Nucleic Acid
                                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHOD OF EXPRESING ANTIFREEZE PROTEINS
                                                                                                                                                                                                                                                                                                                                              US 07/486,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/975,166
                                                                                                                                                                                                                             35,433
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Query Match Best Local Similarity

1.3%;
100.0%;

Score 17; Pred. No.

DB 2; 35;

Length 146;

В

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RESULT
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                                                                                                                   US-09-328-111-577
                                                                       GENERAL
                                                                                       Sequence 577, Appl Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                        Query Match
                                             APPLICANT:
                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: December 16 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 GTGGCAGCGGCGGCGC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                           ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                         36
                                                                                                                                                                                                    58 GTGGCAGCGGCGGCGC 74
                                                                                                                                                                                                                                Local Similarity
mes 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: May 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GIGGCAGCGGCGGC 74
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                      GTGGCAGCGGCGGCGC 20
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37, 66888
                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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  Steinmann, Kathleen E.
Astle, Jon H.
Burgess, Christopher C.
Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Jersey
                                                         Endege, Wilson O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08454720A
                                                                                                   Application US/09328111
                                                                                                                                                                                                                                                                                                                                                                   461 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 Kingsland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.01, version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawasaki,
                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoffman-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                              (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        May 31, 1995
                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Douglas
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                                                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acid
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                                                                                                                                                                                                                                              Score 17;
Pred. No.
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                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                          Length 461;
                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces hygroscopicus US-09-154-083-31
                                                                                    US-09-097-072-1/c
                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1998-09-16
NUMBER OF SEQ. ID NOS: 31
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 31
LENGTH: 718
TYPE: DNA
                                                    Sequence 1, Appris
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches | 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09154083 Patent No. 6150513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for SEQ ID NO 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Polyketide Synthase Enzymes and Recombinant DNA TITLE OF INVENTION: Constructs Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US (EARLIER FILING DATE: 1998-06-10 NUMBER OF SEQ ID NOS: 850
                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 30062-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wu, Kai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                             APPLICANT:
                APPLICANT:
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FILING DATE: 1999-06-08
                                           INFORMATION:
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Lewis, Marcia E.
Monahan, John E.
                                                                   Application US/09097072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll III, Eddie
Lennox, Anna L.
Burnham, Martin K.
                                                                                                                                                                                                    Conservative
                           Kallender, Howard
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MMBER: US/09/154,083
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Pred. No.
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Pred. No.
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TLE OF INVENTION:

Ward, Judith

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RESULT 21
US-08-886-638-1/c
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Best Local Similarity
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PRIOR APPLICATION DATA:
                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                          APPLICANT: Kallender, Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                           203 TACATCGTGTTCATCTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                           991 TACATCGTGTTCATCTG 1007
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              CLASSIFICATION:
                                                                                                         COMPUTER:
                             FILING DATE:
                                                                                      OPERATING SYSTEM:
                                                                                                                                                                COUNTRY:
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                                          APPLICATION NUMBER:
                                                                                                                                                     ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Falk, Stephen T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                   IBM Compatible
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                                          US/08/886,638
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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38;
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us-09-097-072-3/c
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Best Local :
             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                 REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM:
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-994-2488
                                                                                                                                                                                                                                                                               ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                            SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   PRIOR APPLICATION DATA:
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NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: gidB
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                                                                                                               NAME:
                                                                                                                                          FILING DATE:
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                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                               Falk,
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                                          215-994-2222
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Burnham, Martin K. R.
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Pred. No.
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38;
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JS-09-097-072-3

TYPE: nucleic acid
STRANDEDNESS: double

linear

TYPE:

LENGTH:

900 base pairs

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                                                                                          PCT-US91-00899-13
                                                             Sequence 13, Application PC/TUS9100899 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
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          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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  TITLE
                                                  APPLICANT:
                                                                                                                                          991 TACATCGTGTTCATCTG 1007
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                                                                                                                                                                                               Local Similarity
nes 17; Conserv
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                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                  LENGTH:
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  OF INVENTION:
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                                                                                                                                                                                                                                                                                                     nucleic acid
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FastSEQ for Windows Version
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100.0%; Pr
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            Oligosaccharide Structures on Glycoproteins, or as Free Molecules, and For the Isolation
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 Genetic
                                   Method and Products For the Synthesis of
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Building
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Pred. No.
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That Determine These Structur
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PCT-US91-00899-5
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Best Local Similarity
Matches 17; Conserv
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INFORMATION FOR SEQ ID NO:
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                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1068 base pairs
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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NAME: Lavalleye Ph.D., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 GGCAGCGGCGGCGGCAG 310
                                                       APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                  STREET: 1755 Je
CITY: Arlington
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                                 CLASSIFICATION:
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OPERATING SYSTEM: 'PC-DOS/MS-DOS
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ZIP: 22202
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EDNESS: double
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1755 Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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Best Local (
                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 1215 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: unknown
                 MOLECULE TYPE:
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
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MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
-914-281-9
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                                               STRANDEDNESS:
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                                TOPOLOGY:
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17; Conserv
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             DNA (genomic)
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPLOS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.25
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Pred. No.
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Best Local Similarity

1.3%; Score 17; 100.0%; Pred. No.

DB 1; 39;

Length 1488;

Query Match

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В
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US-08-525-058A-9
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Sequence 9, Application US/08525058A Patent. No. 5770420
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
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                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                         714 GGCAGCGGCGGCAG 730
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                                                                                                                                                        60 GGCAGCGGCGGCAG 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 30-MAR-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPOOTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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Pred. No.
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TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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COUNTRY:
22202
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URRENT APPLICATION DATA:
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                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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248855 OPAT UR
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1755 Jefferson Davis Highway,
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE IS
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
               Release #1.0,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CINNER CHAPT CENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                             FILING DATE: 30-MAR APPLICATION NUMBER:
                                                                                  FILING DATE:
                                                                                                                                 CLASSIFICATION:
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(703)486-2347
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                 Version #1.25
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NAMÉ: Lavalleye, Jean-p REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:

2363-060-55

Jean-Paul M. P.

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; MOLECULE TYPE: US-09-042-531-9
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Best Local
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                                                            TELEFAX: (415) 324-09
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                          ORIGINAL SOURCE:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1846 base pair
                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                   RYPOTHETICAL:
                                                                                                  OLECULE TYPE:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714 GGCAGCGGCGGCGGCAG 730
NAME/KEY: CDS
                            INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GGCAGCGGCGGCGGCAG 76
                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 23-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                           : 1846 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1488 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishopric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Webster, Keith A.
                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                        (415) 324-0880
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                                                                                                                                                                                                                                                                                                                                  23-DEC-1994
                                                                                                   cDNA to mRNA
                                                                                                                                   double
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                                                                                                                                                                                                         324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ic, Nanette H.
  Tissue Specific Hypoxia Regulated
  Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; but
100.0%; Pr
                      bcl-2 fusion gene; Seto, et al., EMBO J 7:123 (1988)
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                                                                                                                                                                                                                                                                   38,615
                                                                                                                                                                                                                                                      8255-0018
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Pred. No.
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US-08-365-486A-16
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
                                    FEATURE:
                                                                             ORIGINAL SOURCE:
                                                                                          ANTI-SENSE:
                                                                                                     HYPOTHETICAL:
                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 13-NOV-1995
                                                INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23
CLASSIFICATION:
                                                                                                                                      TOPOLOGY:
                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                             ENGTH:
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17; Cónserv
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                                                                                                                                                              nucleic acid
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350 Cambridge Avenue, Suite 250
CDS
887.,1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, Christopher J.
VENTION: Tissue Specific Hypoxia Regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                   linear
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                                                                                                                                                                                                                                        (415)
                                                                                                         NO
                                                                                                                     cDNA to mRNA
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                                                                                                                                                                                                                                                                                               Charles K
                                                                                                                                                  double
                                                                                                                                                                                                                      324-0960
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                                                                                                                                                                                                                                     324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic Constructs
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                                           bcl-2 fusion gene; Seto, et al., EMBO J 7:123 (1988)
                                                                                                                                                                                                                                                                                                                                                                                     PCT/IB95/00996
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                                                                                                                                                                                                                                                                               . 38, 615
                                                                                                                                                                                                                                                                   8255-0018.30
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Pred. No.
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Local

Similarity

1.3%;

Score 17; ; Pred. No.

DB 4; 39;

Length 1846;

Mismatches

0

Conservative

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PCT-US96-06427-3
                                                                                                                                                               RESULT
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                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              CORRESPONDENCE ADDRESS
                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                 APPLICANT:
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                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                            462 GGCAGCGGCGGCAG 478
                                                                                                                                                                                                                                         60 GGCAGCGGCGGCAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GGCAGCGGCGGCAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lech, Karen F.
NAME: Ton NUMBER: 35,238
                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                  STREET:
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                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                           : 2134 base pairs
nucleic acid
EDNESS: single
Boston
                                                                                                                              Application PC/TUS9606427
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                225 Franklin Street
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                                                                                              The General Hospital Corporation
                                                                                                                                                                                                                                                                       Conservative
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                               Fish & Richardson P.C
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                                                                               FUCOSYLTRANSFERASE GENES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                     Length 2134;
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PCT-US96-06427-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                            OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/483,151
FILING DATE: 07-JUN-1995
                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                              FITLE OF INVENTION:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 GGCAGCGGCGGCGGCAG 478
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                                                                                                COMPUTER:
                                                                                                                                              COUNTRY: UI
                                                                                                                                                                                           CITY: New York
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CLASSIFICATION:
                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08482073
                                                                                                                                                                             New York
                                                                                                                                                                                                          1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2134 base pairs
                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                  ropp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                  Benjamin,
                                                                                                                                                                                                                                                                                                                                                 Osborn, Laurelee
                                                                                                                                                                                                                                                                                                                     Rosa, Margaret D
                                                                                                                                                                                                                                                                                                                                                                                                 Hession,
                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                             z, Susan E
                                                                                                                                                                                                                                                                                                                                                                                 ROY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                Catherine A.
                                                                                                                                                                                                                                                                ADHESION (MILAS)
                                                                                                                                                                                                                                                                                                      ENDOTHELIAL CELL-LEUKOCYTE ADHESION
                                                                                                                                                                                                                                                                                                                                 Christopher D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version
                                                                Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US96/06427
                                 US/08/482,073
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #1.30
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: APPLICATION NUMBER:

31-OCT-1990

US 07/608298 US/08/486,336

APPLICATION NUMBER:

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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10,
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                           SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIOR APPLICATION DATA:
                                                                               ZIP: 10020
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION DATA:
                                                                                                                                                                                                                                 CMBEX OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 GGCAGCGGCGGCAG 522
                                                                                                                                                                                                                DRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GGCAGCGGCGGCAG 76
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APPLICATION NUMBER: FILING DATE:
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 81
                                                                                                                                                                  CITY: New York
                                                                                                                                                                                 STREET:
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                                                                                                                                     COUNTRY:
                                                                                                                                                                                                 ADDRESSEE:
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-8367
                                                                                                                                                   New York
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                                                                                                                                                                                 1251 Avenue of the Americas
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                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                        Goelz, Susan E.
                                                                                                                                                                                                                                                                                                         Benjamin, Christopher D.
                                                                                                                                                                                                                                                                                                                            Osborn, Laurelee
                                                                                                                                                                                                                                                                                                                                                          Lobb, Roy
                                                                                                                                                                                                                                                                                                                                                                          Hession, Catherine
                                                                                                                                                                                                                                                                                              Rosa, Margaret D:
                                           PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                    Fish & Neave
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28-APR-1989
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27-APR-1990
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                                                                                                                                                                                                                                              ADHESION (MILAS)
                                                                                                                                                                                                                                                               MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
                                                                                                                                                                                                                                                                               ENDOTHELIAL CELL-LEUKOCYTE ADHESION
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              US/08/482,073
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08006676B Patent No. 5411865
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                            SOFTWARE: WORD for Windows CURRENT APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, S
TITLE OF INVENTION:
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                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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ELECOMMUNICATION INFORMATION:
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nes 17; Conser
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               NAME: Oster, Jeffrey B.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: RE
                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 15-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                  98040-4906
                                                                                                                                                                                                                                                                                 SSEE: Jeffrey B. I: 8339 SE 57th Mercer Island
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                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2861 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven
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NUMBER: 27,794
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31-OCT-1990
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                                                                                                              US/08/006,676B
                                                                                                                                                                                                                                                                                                    Street
                                                                                                                                                                                                                                                                                                                      Oster
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                 REED-4
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ORGANISM:
US-08-006-676B-2
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Best Local Similarity
Matches 17; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      TELEFAX: (206)233-0644
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3288 CCGAGGAGCGCGCGCG 3304
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A 230Kd Antigen Present in Leishmania TITLE OF INVENTION: Species
                                                                                                                                                                                                                 TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/006,676
                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADUM:
STREET: 51
STRY: Seattle
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                                                                                               OLECULE TYPE:
                                                                                   YPOTHETICAL:
                                                                                                                                                                                                                                                                                     TTORNEY/AGENT INFORMATION:
                                EATURE:
                                                         MMEDIATE SOURCE:
                                                                       NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System 7.1
SOFTWARE: Microsoft Word for Macintosh 5.1a
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,693
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                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
  LOCATION:
                NAME/KEY:
                                                                                                                  POPOLOGY:
                                                                                                                                                        ENGTH:
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CDS
455..3319
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Thehes 17; Conserv
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                                                                 Sequence 2, Application PC/TUS9400324 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                           TITLE OF INVENTION:
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                           NUMBER OF SEQUENCES:
                                                       APPLICANT:
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                                                     Reed, Steven
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(206) 682-6031
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Immunex Corporation
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Steven G.

STEVEN: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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Pred. No. 40;
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COUNTRY:

Seattle

51 University Street

Washington

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Best Local Similarity
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NFORMATION FOR SEQ ID NO: 2:
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ORIGINAL SOURCE:
                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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APPLICATION NUMBER: US/0
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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CLASSIFICATION:
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                                FILING DATE:
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PHILLIPS, DAV
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Apple Macintosh
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US-08-972-719-1
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Best Local Similarity
Matches 17; Conserv
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TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 1:
                                                           INFORMATION FOR SEQ ID NO: 1:
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tent No. 6194557
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                                            SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                               ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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INVOLVED IN INTEGRIN-MEDIATED
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; LOCATION:
US-08-753-038-1
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                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3647 base pairs
2382 GGCAGCGGCGGCGGCAG 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                             Local Similarity nes 17; Conser
                             60 GGCAGCGGCGGCAG 76
                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                  NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                      NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                 (703)486-2347
                                                             Conservative
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                                                                                                                                                                                       unknown
                                                                                                                                                          NO
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                                                                                                                                                                                                                                                                                                                  (703)521-4500
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPPOTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                              Pred.
                                                             Mismatches
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                                                                              No.
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                                                                                         Length 3647;
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RESULT 44

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; MOLECULE TYPE:
; ANTI-SENSE: N
US-08-393-246-7
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                                                                                                                                                 Sequence 7, Application US/08525058A Patent No. 5770420
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                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3647 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                       2382 GGCAGCGGCGGCGGCAG 2398
                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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                                                  TITLE OF
                                                                                  ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                            60 GGCAGCGGCGGCAG 76
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                                                                                                                                    INFORMATION:
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    BLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
    P.C.
    1755 Jefferson Davis Highway, Fourth Floor

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                                                                                                                    LOWE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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OBLON, SPIVAK, McCLELLAND,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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                                                                                                                  JOHN B.
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                                              OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jean-Paul M. P.
                                                                                                  METHODS AND PRODUCTS FOR THE SYNTHESIS
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
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                                                                                                                                                                                                                                                                                                                                               Score 17; Pred. No.
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                                                                                                                                                                                                                                                                                                                                               DB 1;
40;
MAIER & NEUSTADT, P.C
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CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Lavalley, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (703)486-2347
TELEFAX: (703)486-2347
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3647 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                          ; STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ANTI-SENSE: NO US-08-525-058A-7
                                                                                     Query Match 1.3%; Score 17; Best Local Similarity 100.0%; Pred. No. Matches 17; Conservative 0; Mismatc
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/525,058A
FILING DATE:
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22202
                                                                                         Mismatches
                                                                                                                            Length 3647;
                                                                                     Indels
                                                                                   0; Gaps
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Search completed: March 29, 2002, 20:53:54 Job time: 3524 sec